

Result No.	Score	Query			ID	Description
		Match	Length	DB		
1	2282	100.0	2282	6	AR043313	Sequence AR043313
2	2282	100.0	2282	6	AR067737	Sequence AR067737
3	2282	100.0	2282	6	I56851	Sequence I56851
4	2282	100.0	2282	6	AR224830	Sequence AR224830
5	2282	100.0	2282	6	AR403899	Sequence AR403899
6	2282	100.0	2282	6	AR429415	Sequence AR429415
7	2269	99.4	2269	6	AR176322	Sequence AR176322
8	2269	99.4	2269	6	BD271280	Sequence BD271280
9	2269	99.4	2269	6	BD273390	Sequence BD273390
10	2269	99.4	2269	6	AR183468	Sequence AR183468
11	2269	99.4	2269	6	AR183517	Sequence AR183517
12	2269	99.4	2269	6	AR213705	Sequence AR213705
13	2269	99.4	2269	6	AR217276	Sequence AR217276
14	2269	99.4	2269	6	AR282748	Sequence AR282748
15	2269	99.4	2269	6	AR451799	Sequence AR451799
16	2269	99.4	2269	6	AR482244	Sequence AR482244
17	2269	99.4	2269	6	AX042263	Sequence AX042263
18	2269	99.4	2269	6	AX490657	Sequence AX490657
19	2269	99.4	2269	6	AX671082	Sequence AX671082

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Qy	301	TGGACGTGTGTTTGCCCTCAAGTTTGTAAAGTCTGCTGGTTTATTACTGAAAGAAGAATGT	360
Db	301	TGGACGTGTGTTTGCCCTCAAGTTTGTAAAGTCTGCTGGTTTATTACTGAAAGAAGAATGT	360
Qy	361	GGCAGATGTGTTTCTTTACTCTGAGCTGTGATCTTGCTTTGGCGGAGCCCTATAACAAC	420
Db	361	GGCAGATGTGTTTCTTTACTCTGAGCTGTGATCTTGCTTTGGCGGAGCCCTATAACAAC	420
Qy	421	TTCGGAAGAGCATGGCAGCATAGAAAGAAGCAATATCAGGTCAGCATGGGCTCTTGCA	480
Db	421	TTCGGAAGAGCATGGCAGCATAGGAAGAAGCAATATCAGGTCAGCATGGGCTCTTGCA	480
Qy	481	GCTACACTTCTCTCTCGAGAGATGGAACAACTGCGCGCTCTTCTCTCAGGCCCTACGTGT	540
Db	481	GCTACACTTCTCTCTCGAGAGATGGAACAACTGCGCGCTCTTCTCTCAGGCCCTACGTGT	540
Qy	541	CCAATGCTGTGCAGAGGAGCGCGCGCTCGAATACGATGACTCGGTGCAGAGCGTCGAAG	600
Db	541	CCAATGCTGTGCAGAGGAGCGCGCGCTCGAATACGATGACTCGGTGCAGAGCGTCGAAG	600
Qy	601	TGCTGGAGAAATCATCGAATAAACAACTCAGTGGCTTAATGAAGCTTGAGAAATATATCC	660
Db	601	TGCTGGAGAAATCATGGAATAAACAACTCAGTGGCTTAATGAAGCTTGAGAAATATATCC	660
Qy	661	AGGACACATGAGAAGAATAAGTAGAGATACAGCAGATGCAAGTACAGATACAGAACCGACGG	720
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Db	1081	CAGTTCTTCAANAGCAGCACTGATCTCATGGAGCAGTTAATACTTACTGACTATGA	1140
Qy	1141	TGTCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAAGAACAAATCAGTTCA	1200
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Qy	1201	GAGACTGTGTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTAACAT	1260
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Qy	1261	TCCCTAATTTCTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGGAGCGGGT	1320
Db	1261	TCCCTAATTTCTACAGAAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGGAGCGGGT	1320
Qy	1321	GGACAAATTTACGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGCATTTGAAAGAAT	1380
Db	1321	GGACAAATTTACGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGCATTTGAAAGAAT	1380

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LOCUS	AR067737	2282 bp		DNA	linear	PAT 29-SEP-1999	
DEFINITION	Sequence 5 from patent US 5851797.						
ACCESSION	AR067737						
VERSION	AR067737.1 GI:5998959						
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Qy	2041	GCAAGACCCCTAAACATCCATAATTG	TGATTAGACAGAACACCTATGCAAAAGATGAACCG	2100	
Db	2041	GCAAGACCCCTAAACATCCATAATTG	TGATTAGACAGAACACCTATGCAAAAGATGAACCG	2100	
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DEFINITION					
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VERSION					
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KEYWORDS					
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REFERENCE					
1 (bases 1 to 2282)					
AUTHORS					
Davis, S., Jones, P. F. and Yancopoulos, G. D.					
TITLE					
Tie-2 ligand 2					
JOURNAL					
Patent: US 5650490-A 5 22-JUL-1997;					
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ORIGIN					
Query Match 100.0%; Score 2282; DB 6; Length 2282;					
Best Local Similarity 100.0%; Pred. No. 0;					
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
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Db	61	TCCTGGGAGAGAGGAACAAAGACCGTGAAGCTCTCTGTAAAAAGCTGACACGCCCTC	120		
Qy	121	CCAAAGTGACGAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCAATGCTGGAG	180		
Db	121	CCAAAGTGACGAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCAATGCTGGAG	180		
Qy	181	RACACAGAGTAAACCAAGTTTCTCTACTGAAAAGAGGAAGAGAGCTTTTCATTG	240		
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Qy	301	TGGACGTGTGTTTGGCCCTCAAGTTTGCTAAAGCTGCTGGTGTATTAATCTGAAGAAAGATGT	360		

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RESULT 6

AR429415
LOCUS AR429415 2282 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 5 from patent US 6645484.

AR429415

AR429415.1 GI:40189610

KEYWORDS

Unknown.

ORGANISM

Unknown.

REFERENCE

1 (bases 1 to 2282)

AUTHORS

Davis,S., Bruno,J., Goldfarb,M., Aldrich,T.H., Maisonnier,P.C.,
Radziejewski,C., Jones,P.F. and Yancopoulos,G.D.

TITLE Method of blocking blood vessel growth using tie-2 ligand 2									
JOURNAL Patent: US 6645484-A 5 11-NOV-2003;									
FEATURES Location/Qualifiers									
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Query Match 100.0%; Score 2282; DB 6; Length 2282;									
Best Local Similarity 100.0%; Pred. No. 0;									
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2269 bp DNA linear PAT 17-JUL-2003

Cancer treatment using therapeutic conjugates that bind to aminophospholipids.

BD273390.1 GI:33083158

JP 2002520297-A/2.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 2269)

Thorpe, P.E., Ran, S. and Brekken, R.A.

Cancer treatment using therapeutic conjugates that bind to aminophospholipids

Patent: JP 2002520297-A 2 09-JUL-2002;

BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM

OS Homo sapiens (human)

PN JP 2002520297-A/2

PD 09-JUL-2002

PF 12-JUL-1999 JP 2000558846

PR 13-JUL-1998 US 60/092589, 02-DEC-1998 US 60/110600 PI

PC A61K47/48, A61K45/00, A61K49/04, A61P35/00 CC Cancer treatment using therapeutic conjugates that bind to CC

aminophospholipids

PH Key Location/Qualifiers

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1..2269

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99.4%; Score 2269; DB 6; Length 2269;

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DEFINITION Sequence 3 from patent US 6342219.
ACCESSION AR183468
VERSION AR183468.1 GI:20227437
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2269)
AUTHORS Thorpe, P.E. and Brekken, R.A.
TITLE Antibody compositions for selectively inhibiting VEGF
JOURNAL Patent: US 6342219-A 3 29-JAN-2002;
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DEFINITION Sequence 3 from patent US 6342221.
ACCESSION AR183517
VERSION AR183517.1 GI:20227486
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2269)
AUTHORS Thorpe,P.E. and Brekken,R.A.
TITLE Antibody conjugate compositions for selectively inhibiting VEGF
JOURNAL Patent: US 6342221-A 3 29-JAN-2002;
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RESULT 12

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LOCUS Sequence 3 from patent US 6406693.
DEFINITION AR213705
ACCESSION AR213705
VERSION AR213705.1 GI:23310988
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2269)
AUTHORS Thorpe, P.E. and Ran, S.
TITLE Cancer treatment methods using antibodies to aminophospholipids
JOURNAL Patent: US 6406693-A 3 18-JUN-2002;
FEATURES Location/Qualifiers
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Query Match 99.4%; Score 2269; DB 6; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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LOCUS AR217276 2269 bp DNA linear PAT 25-SEP-2002
DEFINITION Sequence 3 from patent US 6416758.
ACCESSION AR217276
VERSION AR217276.1 GI:23316767
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2269)
AUTHORS Thorpe, P.E. and Brekken, R.A.
TITLE Antibody conjugate kits for selectively inhibiting VEGF
JOURNAL Patent: US 6416758-A 3 09-JUL-2002;
FEATURES Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 0;
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QY	1568	AGGACTTACAGGACAGCGGCAAAATAAGCAGCATCAGCCACACAGGAAATGATTTAG	1627
DB	1561	AGGACTTACAGGACAGCGGCAAAATAAGCAGCATCAGCCACACAGGAAATGATTTAG	1620
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DB	1621	CACAAAGGATGGAGACACACGACAAATGTATTGCAAAATGTTCAAAATGCTAAACAGAGG	1680
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DB	1681	CTGGTGGTTGATGCAATGTTCTTCCAACTTTGAAACGGAAATGTACTATCCACAGAGGCA	1740
QY	1748	GAACACAAATTAAGTTCAACGGCAATTAATGGTACTACTGGAAAGGCTCAGGCTATTGCT	1807
DB	1741	GAACACAAATTAAGTTCAACGGCAATTAATGGTACTACTGGAAAGGCTCAGGCTATTGCT	1800
QY	1808	CAAGGCCAACCAACCATGATCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG	1867
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AR282748			
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DEFINITION	Sequence 3 from patent US 6524583.		
ACCESSION	AR282748		
VERSION	AR282748.1		
KEYWORDS	GI:29719451		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 2269)		
AUTHORS	Thorpe, P.E. and Brekken, R.A.		

TITLE Antibody methods for selectively inhibiting VEGF
JOURNAL Patent: US 6524583-A 3 25-FEB-2003;
FEATURES Location/Qualifiers
source 1. .2269
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

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QY	68	AGAGAGAACAAAGGACCTGGAAGCTGCTGTAAAGCTGACACAGCCCTCCCAAGTG	127			
DB	61	AGAGAGAACAAAGGACCTGGAAGCTGCTGTAAAGCTGACACAGCCCTCCCAAGTG	120			
QY	128	AGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGAAACACAG	187			
DB	121	AGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGAAACACAG	180			
QY	188	CAGTAAAAACCAAGTTTGCTACTGGAAGAAAGGAAAGAGAGACTTTCATTTGACGGACC	247			
DB	181	CAGTAAAAACCAAGTTTGCTACTGGAAGAAAGGAAAGAGAGACTTTCATTTGACGGACC	240			
QY	248	CAGCCATGCGCAGCTAGCAGCCCTCGTTTTCAGCGGACGAGCTCGGACCTCGGAGCT	307			
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DB	361	TGTTTTCTTTACTCGAGCTGTGATCTGTCTTGGCGGAGCTATTAACAACCTTTCGGAA	420			
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QY	488	TTTCTCTCTCCAGAGATGGACAACTGCGCGCTCTTCTCCAGCCCTACGTTGCCAATGC	547			
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DB	601	GAACATCATGGAAGAAACAACACTCAGTGGCTAATGAAGCTTGAGAAATATATCCAGGACAA	660			
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DB	661	CATGAAGAAAGAAATGGTAGAGATACAGCAGAATGCAGTACAGAACCCAGCGGCTGTGAT	720			
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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- 13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	2269	99.4	2269	3 AAZ92213	Aaz92213 Human ang
6	2269	99.4	2269	3 AAC67774	Aac67774 Human ang
7	2269	99.4	2269	5 AAS70958	Aas70958 DNA encod
8	2269	99.4	2269	6 ABZ35349	Abz35349 Human gen
9	2269	99.4	2269	6 ABK47716	Abk47716 DNA encod
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11	2269	99.4	2269	11 ADN95380	Adn95380 Human BEC
12	2269	99.4	2269	12 ADO28674	Ado28674 Human TIE
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16	2233.6	97.9	2384	10 ADI02709	Adi02709 Human cdn
17	2230.4	97.7	3251	8 ABX63024	Abx63024 Human cdn
18	2219	97.2	2227	12 ADQ09386	Adq09386 Human ang
19	2197	96.3	2624	4 AAK94849	Aak94849 Human ful
20	2197	96.3	2624	12 ADL31981	Adl31981 Full leng

21	1849.2	81.0	3533	5 AAS75801	Aas75801 DNA encod
22	1290.6	56.6	1500	2 AAV18616	Aav18616 Nucleotid
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24	1210	53.0	1376	12 ADQ09387	Adq09387 Human ang
25	1186.6	52.0	1387	8 AAD49987	Aad49987 Human ang
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28	1094.8	48.0	1506	8 AAD49995	Aad49995 Human ang
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39	595.6	26.1	240825	6 ABQ81802	Abq81802 Human PG-
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45	550.2	24.1	1494	9 AAD58428	Aad58428 Human ang

ALIGNMENTS

RESULT 1
AAT14650

ID: AAT14650 standard; DNA; 2282 BP.

XX AAT14650;

DT 28-OCT-1996 (first entry)

Human TIE-2 ligand 2-encoding DNA derived from pBluescript KS clone.

XX Angiogenesis; neovascularisation; tumour development; wound healing; TIE;
XX tyrosine kinase with Ig and EGF homology domains; vector; recombinant;
XX clone; diagnosis; ischaemia; thromboembolytic disease; atherosclerosis;
XX inflammation; diabetes; ligand bodies; delivery; targeting; ss.

OS Homo sapiens.

XX Key Location/Qualifiers
XX CDS 357..1847

XX FT /*tag= a

XX WO9611269-A2.

XX 18-APR-1996.

XX 06-OCT-1995; 95WO-US012935.

XX 07-OCT-1994; 94US-00319932.

XX 27-OCT-1994; 94US-00330261.

XX 02-DEC-1994; 94US-00348492.

XX 09-DEC-1994; 94US-00353503.

XX 17-JAN-1995; 95US-00373579.

XX 06-APR-1995; 95US-00418595.

XX (REG-) REGENERON PHARM INC.

XX Davis S, Bruno J, Goldfarb M, Aldrich TH, Maisompierre PC;
XX Radziejewski C, Jones PF, Yancopoulos GD;

XX WPI; 1996-209850/21.

XX P-PSDB; AAR94605.

XX Nucleic acid encoding TIE-2 ligand and related vectors - useful in

PT diagnosis and treatment of neovascularisation, tumours, etc., or to
PT promote wound healing, etc.

Claim 2; Fig 6; 84pp; English.

AAT14650 is a portion of a pBluescript KS clone encoding the human TIE-2 (hTIE-2) ligand 2. hTIE-2 ligand DNAs of the invention are recombinant versions of the native ligand coding sequences and may be used to produce the ligands at a high yield. Antibodies and receptor bodies that bind to TIE-2 ligands may be used to inhibit angiogenesis and neovascularisation (e.g. associated with tumour development) and the TIE-2 ligands themselves are useful to promote neovascularisation and wound healing e.g. for treatment of ischaemia. TIE-2 ligands are also useful to treat thromboembolytic disease, atherosclerosis, inflammation and diabetes. Ligand bodies contg. TIE-2 ligands may also be useful for the delivery and -targeting of growth factors, toxins etc. to sites where their presence is advantageous

Sequence 2282 BP; 746 A; 498 C; 520 G; 518 T; 0 U; 0 Other;

Query Match 100.0%; Score 2282; DB 2; Length 2282;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	61	TCGTGGGAGAGGAGCAAGACCGTGAAGCTCTCTGTAAGACGTACACAGCCCTC	120
DB	61	TCGTGGGAGAGGAGCAAGACCGTGAAGCTCTCTGTAAGACGTACACAGCCCTC	120
QY	121	CCAAGTGAGCAGGACTGTTCTTCCACCTGCAATCTGACAGTTTACTGTCATGCTGGAG	180
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QY	361	GGCAGATGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAAT	420
DB	361	GGCAGATGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAAT	420
QY	421	TTTCGGAAGAGCATGACAGCATAGGAAGAACAATATCAGGTCCAGCATGGTCTCTGCA	480
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QY	541	CCAAATGCTGTGAGAGGAGCGCGCTCGAATACAGTACGTCTGGTGCAGAGGCTGCAAG	600
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DB	661	AGGACAAACATGAAGAAAGAAATGGTAGAGATACAGCAGAAATCAGTACAGAACCCAGCG	720
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DB	961	ACATCATCAACTCAGTCAATATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCA	1020
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DB	1081	CAGTTCTTCAAAAGCAGCAACATGATCTCATGGACAGTAACTTACTGACTATGA	1140
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DB	1141	TGTCCACATCAAACTCAGTAAAGACCCACCTGTTGCTAAAGAAAGAAACAAATCAGCTTCA	1200
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DB	1201	GAGACTGTGCTGAAGTATTCAAAATCAGGACACACACAATAATGGCATCTACAGTTAAAT	1260
QY	1261	TCCCTAAATTTCTACAGAGAGATCAAGGCTCTAGTGACATGGAAGCTGGAGAGCGGT	1320
DB	1261	TCCCTAAATTTCTACAGAGAGATCAAGGCTCTAGTGACATGGAAGCTGGAGAGCGGT	1320
QY	1321	GGACAAATTAATTCAGCGCATGAGGATGGCAGCTTGTATTTTCAGAGGACTTGGAAAGAT	1380
DB	1321	GGACAAATTAATTCAGCGCATGAGGATGGCAGCTTGTATTTTCAGAGGACTTGGAAAGAT	1380
QY	1381	ATAAAGTGGATTTGGTAAACCTTTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCG	1440
DB	1381	ATAAAGTGGATTTGGTAAACCTTTCAGGAGAAATATGGCTGGGAAATGAGTTTGTTCG	1440
QY	1441	AACTGACTTAATCAGCAACGCTATGCTTAAATAACACCTTAAAGACTGGGAAGGAAATG	1500
DB	1441	AACTGACTTAATCAGCAACGCTATGCTTAAATAACACCTTAAAGACTGGGAAGGAAATG	1500
QY	1501	AGGCTTACTCAATTTGATGAACAATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGATT	1560
DB	1501	AGGCTTACTCAATTTGATGAACAATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGATT	1560
QY	1561	ACCTTAAAGACTTACAGGAGCAGCCGCAAAATAAGCAGCATCAGCCAAACAGGAAATG	1620
DB	1561	ACCTTAAAGACTTACAGGAGCAGCCGCAAAATAAGCAGCATCAGCCAAACAGGAAATG	1620
QY	1621	ATTTTAGCACAAGAGATGGAGACGACCAATGATTTTGGAAATGTTTCACAAATGCTAA	1680
DB	1621	ATTTTAGCACAAGAGATGGAGACGACCAATGATTTTGGAAATGTTTCACAAATGCTAA	1680
QY	1681	CAGGAGGCTGGTGGTTCATGATGATGCTTCTTCCAACTTGAACGGAATGTACTATCCAC	1740
DB	1681	CAGGAGGCTGGTGGTTCATGATGATGCTTCTTCCAACTTGAACGGAATGTACTATCCAC	1740
QY	1741	AGAGCAGAACACAAATTAAGTTCAACGGCATTAATATGTTACTCTGGAAGAGCTCAGGCT	1800
DB	1741	AGAGCAGAACACAAATTAAGTTCAACGGCATTAATATGTTACTCTGGAAGAGCTCAGGCT	1800
QY	1801	ATTGCTCAGGCCACACCATGATGATCCGACAGCAGATTTCTTAAACATCCCAAGTCCA	1860

|||||
781 TAACTGATGTGAAGCCCAAGTATTAAATCAGACCACGAGACTTGAACTTCAGCTCTTGG 840
|||||
841 AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAGACCGAGTGAATAA 900
|||||
841 AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCAGACCGAGTGAATAA 900
|||||
901 ACAAAATTGCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGACAAGC 960
|||||
901 ACAAAATTGCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGTAGCTATGGAAGACAAGC 960
|||||
961 ACATCATCCAACTACAGTCAATAAAGAAAGAAAGATCAGCTACAGGTGTGTAGTATCCA 1020
|||||
961 ACATCATCCAACTACAGTCAATAAAGAAAGAAAGATCAGCTACAGGTGTGTAGTATCCA 1020
|||||
1021 AGCAAAATTCATTTGAAGAACTAGAAAAAATAATAGTGTGCTGCCCGGTGAATAATT 1080
|||||
1021 AGCAAAATTCATTTGAAGAACTAGAAAAAATAATAGTGTGCTGCCCGGTGAATAATT 1080
|||||
1081 CAGTTCTTCAAAGCAGCAACATGATCTCATGGAGACAGTTAATACCTTACTGACTATGA 1140
|||||
1081 CAGTTCTTCAAAGCAGCAACATGATCTCATGGAGACAGTTAATACCTTACTGACTATGA 1140
|||||
1141 TGTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAAAGAAACAAATCAGCTTCA 1200
|||||
1141 TGTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAAAGAAACAAATCAGCTTCA 1200
|||||
1201 GAGACTGTCTGAAGTATTCAAATCAGGACACACCAAAATGSCATCTACAGTTAAACAT 1260
|||||
1201 GAGACTGTCTGAAGTATTCAAATCAGGACACACCAAAATGSCATCTACAGTTAAACAT 1260
|||||
1261 TCCCTAAATTTCTACAGAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGAGCGGGT 1320
|||||
1261 TCCCTAAATTTCTACAGAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGAGCGGGT 1320
|||||
1321 GGACAAATTTATCAGGACCTGAGAGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAAT 1380
|||||
1321 GGACAAATTTATCAGGACCTGAGAGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAAT 1380
|||||
1381 ATAAAGTGGATTGTGTAACCTTCAAGGAGATATTTGGCTGGGAAATGATGTTGTTTCGC 1440
|||||
1381 ATAAAGTGGATTGTGTAACCTTCAAGGAGATATTTGGCTGGGAAATGATGTTGTTTCGC 1440
|||||
1441 AACTGACTAATCAGCAACGCTATGTCTTAAATAACACCTTAAAGACTGGGAAGGAAATG 1500
|||||
1441 AACTGACTAATCAGCAACGCTATGTCTTAAATAACACCTTAAAGACTGGGAAGGAAATG 1500
|||||
1501 AGGCTTACTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGATTC 1560
|||||
1501 AGGCTTACTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGATTC 1560
|||||
1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATAAGCAGCATCAGCCAAACAGGAAATG 1620
|||||
1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATAAGCAGCATCAGCCAAACAGGAAATG 1620
|||||
1621 ATTTTAGCAAAAGGATGGAGACAACGAAATGATTTTGCAAAATGTTTCAAAAATGCTAA 1680
|||||
1621 ATTTTAGCAAAAGGATGGAGACAACGAAATGATTTTGCAAAATGTTTCAAAAATGCTAA 1680
|||||
1681 CAGGAGGCTGGTGTGATGATGTGCTTCCAACTTGAACGGAATGTTACTATCCAC 1740
|||||
1681 CAGGAGGCTGGTGTGATGATGTGCTTCCAACTTGAACGGAATGTTACTATCCAC 1740
|||||
1741 AGAGGACAGAACAAATAAGTTCAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCT 1800
|||||
1741 AGAGGACAGAACAAATAAGTTCAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCT 1800
|||||
1801 ATTCGCTCAAGGCCCAACCATGATGATCCGACAGAGATTTCTTAAACATCCAGTCCA 1860
|||||
1801 ATTCGCTCAAGGCCCAACCATGATGATCCGACAGAGATTTCTTAAACATCCAGTCCA 1860
|||||
1861 CTTGAGGAGCTGCTCGACTATTCTTCAAGACTTAAGCCAGTCACTGAAGTCAGG 1920
|||||

Db 1861 CTTGAGGAACCTGCTCTCGAACTATTTTCAAGACTTTAAGCCCACTGCACTGAAAAGTCACGG 1920
QY 1921 CTGCGCACTGTCTCTCTCTTCCACCACAGAGGCGGTGCTCGGTGCTGACGGGACCCACA 1980
Db 1921 CTGCGCACTGTCTCTCTTCCACCACAGAGGCGGTGCTCGGTGCTGACGGGACCCACA 1980
QY 1981 TGCTCCAGATTAGAGCCGTGTAACCTTTATCACTTTAAACTTTGTCATCACTTTAAACGGACCAA 2040
Db 1981 TGCTCCAGATTAGAGCCGTGTAACCTTTATCACTTTAAACTTTGTCATCACTTTAAACGGACCAA 2040
QY 2041 GCAAGACCCCTAAACATCATTAATTTGATTAGACAGAACACCTATGCAAGATGAACCG 2100
Db 2041 GCAAGACCCCTAAACATCATTAATTTGATTAGACAGAACACCTATGCAAGATGAACCG 2100
QY 2101 AGGCTGAGAATCAGACTGACAGCTTTTACAGAGCTGCTGTCAACCAAGAAATGTTATGTG 2160
Db 2101 AGGCTGAGAATCAGACTGACAGCTTTTACAGAGCTGCTGTCAACCAAGAAATGTTATGTG 2160
QY 2161 CAAAGTTTATCAGTAAATAAATCTGGAACACAGACACTTATGTTTATACAAATACAGATCATCT 2220
Db 2161 CAAAGTTTATCAGTAAATAAATCTGGAACACAGACACTTATGTTTATACAAATACAGATCATCT 2220
QY 2221 TGGAACTGCAATCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280
Db 2221 TGGAACTGCAATCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280
QY 2281 TC 2282
Db 2281 TC 2282
RESULT 3
AAV18619
ID AAV18619 standard; DNA; 2282 BP.
XX AAV18619;
AC AAV18619;
DT 09-SEP-1998 (first entry)
XX Human TIE-2 ligand 2 from clone pbluescript KS.
DE Chimeric TIE ligand 2N1C1F; TIE-2 ligand; neovascularisation; tumour;
KW human; ss.
XX Homo sapiens.
OS
XX Key Location/Qualifiers
FH CDS 357..1847
FT /*tag= a
FT /note= "human TIE-2 ligand 2"
XX
PN W09805779-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-US013557.
XX
PR 02-AUG-1996; 96US-0022999p.
PR 25-OCT-1996; 96US-00740223.
XX
PA (REGE-) REGENERON PHARM INC.
XX
PI Davis S, Yancopoulos GD;
XX
DR WPI; 1998-145615/13.
DR P-PSDB; AAW47532.
XX
PT Modified human TIE-2 receptor ligand(s) - useful for promoting wound
PT healing.
XX
PS Example 8; Fig 6; 202pp; English.
XX
CC This is the nucleotide sequence of the human TIE-2 ligand 2, used in the

CC method of the invention, involving the production of TIE-2 ligands which
CC promote healing. The nucleic acids, vectors and host cells used in the
CC method of the invention are useful for the recombinant production of the
CC ligands. The ligands, etc. are useful for blocking blood vessel growth,
CC promoting neovascularisation, promoting the growth or differentiation of
CC a cell expressing the TIE receptor, blocking the growth or
CC differentiation of a cell expressing the TIE receptor and for attenuating
CC or preventing tumour growth in a human
XX
SQ Sequence 2282 BP; 746 A; 497 C; 520 G; 519 T; 0 U; 0 Other;

Query Match 99.9%; Score 2280.4; DB 2; Length 2282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2281; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAATTCCTGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60
DB 1 GAATTCCTGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60

QY 61 TCTGGGAGAGAGAAACAAGGACCGTGAAGCTGCTCTTAAAGCTGACACAGCCCTC 120
DB 61 TCTGGGAGAGAGAAACAAGGACCGTGAAGCTGCTCTTAAAGCTGACACAGCCCTC 120

QY 121 CCAAGTGAGCAGACTGTTCTTCCACTGCAATCTGACAGTTTACTGTCATGCCCTGGAG 180
DB 121 CCAAGTGAGCAGACTGTTCTTCCACTGCAATCTGACAGTTTACTGTCATGCCCTGGAG 180

QY 181 AACACAGCAGTAAACCCAGTTTGTCTGGAAGAGGAAAGAGAACTTTCATTG 240
DB 181 AACACAGCAGTAAACCCAGTTTGTCTGGAAGAGGAAAGAGAACTTTCATTG 240

QY 241 ACGGACCCAGCCTAGCAGCGCTAGCAGCCCTGCGTTTTCAGACGCGCAGCAGCTCGG 300
DB 241 ACGGACCCAGCCTAGCAGCGCTAGCAGCCCTGCGTTTTCAGACGCGCAGCAGCTCGG 300

QY 301 TGAACGCTGTTGGCCCTCAAGTTTGTCTGGAAGAGGAAAGAGAACTTTCATTG 360
DB 301 TGAACGCTGTTGGCCCTCAAGTTTGTCTGGAAGAGGAAAGAGAACTTTCATTG 360

QY 361 GGCAGATGTTTCTTACTCTGAGCTGTGANTCTTGTCTTGGCCGAGCCTTAAACACT 420
DB 361 GGCAGATGTTTCTTACTCTGAGCTGTGANTCTTGTCTTGGCCGAGCCTTAAACACT 420

QY 421 TTCCGAAGAGCATGGACAGCATAGGAAGAGCAATATCAGTCCAGCATGGGTCTGCA 480
DB 421 TTCCGAAGAGCATGGACAGCATAGGAAGAGCAATATCAGTCCAGCATGGGTCTGCA 480

QY 481 GCTACACTTCTCTCCAGAGATGGACAACTGCGCGCTCTTCTCCAGCCCTTACGTT 540
DB 481 GCTACACTTCTCTCCAGAGATGGACAACTGCGCGCTCTTCTCCAGCCCTTACGTT 540

QY 541 CCAATGCTGTGAGAGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTGCAAG 600
DB 541 CCAATGCTGTGAGAGGAGCGCGCTCGAATACGATGACTCGGTGCAGAGGCTGCAAG 600

QY 601 TGCTGGAGAACATCATGGAACAACTCACTGAGTGGCTTAATGAAGCTTGAAGTATATCC 660
DB 601 TGCTGGAGAACATCATGGAACAACTCACTGAGTGGCTTAATGAAGCTTGAAGTATATCC 660

QY 661 AGGACAACTGAAGAAAGAAATGTTAGATACAGCAGAAATGCAAGTACAGAACGAG 720
DB 661 AGGACAACTGAAGAAAGAAATGTTAGATACAGCAGAAATGCAAGTACAGAACGAG 720

QY 721 CTGTGATGATAGAAATAGGGAACAACCTGTTGAACCAACAGCTGAGCAACGCGGA 780
DB 721 CTGTGATGATAGAAATAGGGAACAACCTGTTGAACCAACAGCTGAGCAACGCGGA 780

QY 781 TAACGTGATGGAAGCCCAAGTATTAATCAGACACGAGACTTGAACCTTCAGCTCTGG 840
DB 781 TAACGTGATGGAAGCCCAAGTATTAATCAGACACGAGACTTGAACCTTCAGCTCTGG 840

QY 841 AACACTCCCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAGACCACTGTA 900
DB 841 AACACTCCCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAGACCACTGTA 900

DB 841 AACACTCCCTCTCGACAAACAAATTTGGAAGAAACAGATTTTGGACCAGACCACTGTA 900
QY 901 ACAAAATTGCAAGATAGAACAGTTTCTTAGAAAAGAGGTGCTAGCTATGGAAGACAAGC 960
DB 901 ACAAAATTGCAAGATAGAACAGTTTCTTAGAAAAGAGGTGCTAGCTATGGAAGACAAGC 960

QY 961 ACATCATCAACTACAGTCAATTAAGAAAGAGAAAGATCAGCTACAGGTGTTAGTATCCA 1020
DB 961 ACATCATCAACTACAGTCAATTAAGAAAGAGAAAGATCAGCTACAGGTGTTAGTATCCA 1020

QY 1021 AGCAAAATTTCCATCATTTGAAGAACTAGAAAAAAAATAGTGAAGTCCACCGTGAATTA 1080
DB 1021 AGCAAAATTTCCATCATTTGAAGAACTAGAAAAAAAATAGTGAAGTCCACCGTGAATTA 1080

QY 1081 CAGTTCTTCAAAAGCAGCAACATGATCTCATGAGACAGTTAATACTTACTGACTATGA 1140
DB 1081 CAGTTCTTCAAAAGCAGCAACATGATCTCATGAGACAGTTAATACTTACTGACTATGA 1140

QY 1141 TGTCACATCAAACTCAGCTTAAGGACCCCACTGTTGCTAAGAGAAACAAATCAGCTTCA 1200
DB 1141 TGTCACATCAAACTCAGCTTAAGGACCCCACTGTTGCTAAGAGAAACAAATCAGCTTCA 1200

QY 1201 GAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACACGTTAA 1260
DB 1201 GAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACACGTTAA 1260

QY 1261 TCCTTAATTTACAGAAAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGCT 1320
DB 1261 TCCTTAATTTACAGAAAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGCT 1320

QY 1321 GGAACAATTTACAGCAGCTGAGGATGGGACGCTTGAATTTTTCAGAGGACTTGGAAAGA 1380
DB 1321 GGAACAATTTACAGCAGCTGAGGATGGGACGCTTGAATTTTTCAGAGGACTTGGAAAGA 1380

QY 1381 ATAAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTTCGC 1440
DB 1381 ATAAAGTGGGATTTGGTAAACCTTTCAGGAGAAATATTGGCTGGGAAATGAGTTTTCGC 1440

QY 1441 AACTGACTAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAAAGGAATG 1500
DB 1441 AACTGACTAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGACTGGGAAAGGAATG 1500

QY 1501 AGGCTTACTCATTTGATGAACATTTCTCTCTCAAGTGAAGACTCAATTTATAGGATTC 1560
DB 1501 AGGCTTACTCATTTGATGAACATTTCTCTCTCAAGTGAAGACTCAATTTATAGGATTC 1560

QY 1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATTAAGCAGCATCAGCCAAACCCAGGAAATG 1620
DB 1561 ACCTTAAAGGACTTACAGGACAGCGGCAAAATTAAGCAGCATCAGCCAAACCCAGGAAATG 1620

QY 1621 ATTTTAGCAAAAAGGATGGAGACACGACAAATGTATTTGCAAAATGTTCAAAATGCTAA 1680
DB 1621 ATTTTAGCAAAAAGGATGGAGACACGACAAATGTATTTGCAAAATGTTCAAAATGCTAA 1680

QY 1681 CAGAGGCTGGTGGTTGATGCAATGCTCTTCCAACTTTGAACGGATGTTACTATCCAC 1740
DB 1681 CAGAGGCTGGTGGTTGATGCAATGCTCTTCCAACTTTGAACGGATGTTACTATCCAC 1740

QY 1741 AGAGGACAGACAAATAAGTTCAACGGCATTAATGTTACTCTGGAAGGCTCAGGCT 1800
DB 1741 AGAGGACAGACAAATAAGTTCAACGGCATTAATGTTACTCTGGAAGGCTCAGGCT 1800

QY 1801 ATTTCGCTCAAGGGCCAAACCATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCA 1860
DB 1801 ATTTCGCTCAAGGGCCAAACCATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCA 1860

QY 1861 CCTGAGGAACTGTCTCGAACTATTTTCAAGAGCTTAAGCCAGTGCATGGAAGTCAAGG 1920
DB 1861 CCTGAGGAACTGTCTCGAACTATTTTCAAGAGCTTAAGCCAGTGCATGGAAGTCAAGG 1920

QY 1921 CTGGGCACTGTGCTCTTCCACACAGAGGGGCTGTCTGGTGTGACGGGACCCACA 1980
DB 1921 CTGGGCACTGTGCTCTTCCACACAGAGGGGCTGTCTGGTGTGACGGGACCCACA 1980

SQ		Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;	
Query Match		99.4%; Score 2269; DB 3; Length 2269;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 2269; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
QY	8	TGGGTTGGTGTATATCTCTCCAGCCTTTGAGGGAGGGAACAACACTGTAGGATCTGGGG	67
DB	1	TGGGTTGGTGTATATCTCTCCAGCCTTTGAGGGAGGGAACAACACTGTAGGATCTGGGG	60
QY	68	AGAGAGGAACAAGACCGGTGAAGCTCTCTGTAAAGCTCACACAGCCCTCCCAAGTG	127
DB	61	AGAGAGGAACAAGACCGGTGAAGCTCTCTGTAAAGCTCACACAGCCCTCCCAAGTG	120
QY	128	AGCAGACTGTTTCTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGAGAACACAG	187
DB	121	AGCAGACTGTTTCTCCCACTGCAATCTGACAGTTTACTGCAATGCTGAGAGAGAACACAG	180
QY	188	CAGTAAAAACCAAGTTTGCTACTGGAAAAAGAGGAAGAAGACTTTTCATTGACGGACC	247
DB	181	CAGTAAAAACCAAGTTTGCTACTGGAAAAAGAGGAAGAAGACTTTTCATTGACGGACC	240
QY	248	CAGCCATGCGAGGTAGCAGCCCTGGTTTTCAGAGGCGAGAGCTCGGACTCTCGAAGT	307
DB	241	CAGCCATGCGAGGTAGCAGCCCTGGTTTTCAGAGGCGAGAGCTCGGACTCTCGAAGT	300
QY	308	GTGTTTGCCTCAAGTTTGTAAAGTGTCTGTTTAACTGAAGAAAGAAATGTGCAGAT	367
DB	301	GTGTTTGCCTCAAGTTTGTAAAGTGTCTGTTTAACTGAAGAAAGAAATGTGCAGAT	360
QY	368	TGTTTTCTTTACTCTGAGCTGTGATCTTGCTTTGGCCGAGCTTATAACAATTTTCGGAA	427
DB	361	TGTTTTCTTTACTCTGAGCTGTGATCTTGCTTTGGCCGAGCTTATAACAATTTTCGGAA	420
QY	428	GAGCATGACGATAGGAAGAACAATATCAGTTCAGATGGTCTCGAGCTACAC	487
DB	421	GAGCATGACGATAGGAAGAACAATATCAGTTCAGATGGTCTCGAGCTACAC	480
QY	488	TTTTCTCTCTGCGAGAGATGGACAACTGCGCGTCTTCTCCAGCCCTACGTTCCAAATGC	547
DB	481	TTTTCTCTCTGCGAGAGATGGACAACTGCGCGTCTTCTCCAGCCCTACGTTCCAAATGC	540
QY	548	TGTGACAGAGGACGGCCCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTGTCTGA	607
DB	541	TGTGACAGAGGACGGCCCGCTCGAATACGATGACTCGGTGCGAGGCTGCAAGTGTCTGA	600
QY	608	GAACTATGGAAGAAACAACACTCAGTGGCTAATGAAGCTTGAGATTTATATCCAGGACA	667
DB	601	GAACTATGGAAGAAACAACACTCAGTGGCTAATGAAGCTTGAGATTTATATCCAGGACA	660
QY	668	CATGAAGAAAGAAATGGTAGAGATACAGAGAAATGCAATGCAAGAACACAGCCGCTGTGAT	727
DB	661	CATGAAGAAAGAAATGGTAGAGATACAGAGAAATGCAATGCAAGAACACAGCCGCTGTGAT	720
QY	728	GATAGAAATAGGGAACAACCTTGTGAACCAACAGCTGAGGAAACCGGGAAGTTAACTGA	787
DB	721	GATAGAAATAGGGAACAACCTTGTGAACCAACAGCTGAGGAAACCGGGAAGTTAACTGA	780
QY	788	TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCAGCTCTTGGAACTCTC	847
DB	781	TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGACTTGAACCTTCAGCTCTTGGAACTCTC	840
QY	848	CCTCTCGAACAACAAATTTGGAAAAACAGATTTTGGACCAAGACAGCTGGAATTAACAAAT	907
DB	841	CCTCTCGAACAACAAATTTGGAAAAACAGATTTTGGACCAAGACAGCTGGAATTAACAAAT	900
QY	908	GCAAGATAAGAACAGTTTCTTAGAAAGAAAGGTGCTAGCTATGGAAGAACAGCAATCAT	967
DB	901	GCAAGATAAGAACAGTTTCTTAGAAAGAAAGGTGCTAGCTATGGAAGAACAGCAATCAT	960
QY	968	CCAACTTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTTGTAGTATCCAAAGAAAA	1027
DB	961	CCAACTTACAGTCAATAAAGAGAGAAAGATCAGCTTACAGGTTGTAGTATCCAAAGAAAA	1020
1028		TTCCATCATTTGAAGAACTAGAAAAAATAATAGTACTGTCACCGTGAATAATTCAGTTCT	1087
1021		TTCCATCATTTGAAGAACTAGAAAAAATAATAGTACTGTCACCGTGAATAATTCAGTTCT	1080
1088		TCAAAAGCAGCAACATGATCTCATGAGACAGTGTAACTTACTGACTATGATGTCCAC	1147
1081		TCAAAAGCAGCAACATGATCTCATGAGACAGTGTAACTTACTGACTATGATGTCCAC	1140
1148		ATCAAACTCAGTAAAGACCCACCTGTTCTTAAAGAAACAATAACAGCTTCAGAGACTG	1207
1141		ATCAAACTCAGTAAAGACCCACCTGTTCTTAAAGAAACAATAACAGCTTCAGAGACTG	1200
1208		TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCCTAA	1267
1201		TGCTGAAGTATTCAAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCCTAA	1260
1268		TTCTACAGAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGCGGTGACAAAT	1327
1261		TTCTACAGAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGCGGTGACAAAT	1320
1328		TATTTCAGAGAGTGAAGATGTCAGGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT	1387
1321		TATTTCAGAGAGTGAAGATGTCAGGTTGATTTTCAGAGGACTTGGAAAGAAATAAAGT	1380
1388		GGGATTTGGTAAACCTTCAGGAGATATTGGCTGGGAAATGAGTTTGTTCGCAACTGCAC	1447
1381		GGGATTTGGTAAACCTTCAGGAGATATTGGCTGGGAAATGAGTTTGTTCGCAACTGCAC	1440
1448		TAAATCAGCAACGCTATGCTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTA	1507
1441		TAAATCAGCAACGCTATGCTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTA	1500
1508		CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTAGATTCACCTTAA	1567
1501		CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTAGATTCACCTTAA	1560
1568		AGGACTTACAGGACAGCCCGCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTAG	1627
1561		AGGACTTACAGGACAGCCCGCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTAG	1620
1628		CACAAAGATGGAGACACGAAATGATTTGCAATGTTTCAAAATGTTCAAAATGCTTAACAGG	1687
1621		CACAAAGATGGAGACACGAAATGATTTGCAATGTTTCAAAATGTTCAAAATGCTTAACAGG	1680
1688		CTGGTGTGTTGATGATGTTGCTTCCAACTTGAACGGAATGTACTTCAACAGAGCA	1747
1681		CTGGTGTGTTGATGATGTTGCTTCCAACTTGAACGGAATGTACTTCAACAGAGCA	1740
1748		GAACACAAATAGTTTCAACGGCATTTAAATGGTACTTCTGGAAGGCTCAGGCTATTCGCT	1807
1741		GAACACAAATAGTTTCAACGGCATTTAAATGGTACTTCTGGAAGGCTCAGGCTATTCGCT	1800
1808		CAAGGCCAACCATGATGATCCGACAGCAGATTTCTTAAACATCCCATCCACCTGAGG	1867
1801		CAAGGCCAACCATGATGATCCGACAGCAGATTTCTTAAACATCCCATCCACCTGAGG	1860
1868		AATGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCATCTGAAAGTCAAGGCTGCGCA	1927
1861		AATGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCATCTGAAAGTCAAGGCTGCGCA	1920
1928		CTGTGCTCTTCTTCCACCAAGAGGCGGTGCTGGTGTCTGACGGGACCCCATGCTCCA	1987
1921		CTGTGCTCTTCTTCCACCAAGAGGCGGTGCTGGTGTCTGACGGGACCCCATGCTCCA	1980
1988		GATTAGAGCCGTAAATTTTATCACTTAAATGTCATCACTTAAACATCCCATCCAGCAAGAC	2047
1981		GATTAGAGCCGTAAATTTTATCACTTAAATGTCATCACTTAAACATCCCATCCAGCAAGAC	2040
2048		CCTTAAACATCCATATTTGTTAGTACAGAAACACCTATGCAAAAGATGAACCCGAGGCTGA	2107
2041		CCTTAAACATCCATATTTGTTAGTACAGAAACACCTATGCAAAAGATGAACCCGAGGCTGA	2100

QY	1208	TGCTGAAGTATTCAAAATCAGGACACACCACAAATGGCATCTACAGTTAACTTCCCTAA	1267
Db	1201	TGCTGAAGTATTCAAAATCAGGACACACCACAAATGGCATCTACAGTTAACTTCCCTAA	1260
QY	1268	TTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGGACAAAT	1327
Db	1261	TTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGGACAAAT	1320
QY	1328	TATTACAGCCACTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGT	1387
Db	1321	TATTACAGCCACTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGT	1380
QY	1388	GGGATTTGGTAAACCCCTTCAGGAGAAATATTTGGCTGGGAATGAGTTTGTTCGCAACTGCAC	1447
Db	1381	GGGATTTGGTAAACCCCTTCAGGAGAAATATTTGGCTGGGAATGAGTTTGTTCGCAACTGCAC	1440
QY	1448	TAATCAGCAACCGCTATGTCTTAAATAACACCTTAAAGCTGGGAAGGGAATGAGGCTTA	1507
Db	1441	TAATCAGCAACCGCTATGTCTTAAATAACACCTTAAAGCTGGGAAGGGAATGAGGCTTA	1500
QY	1508	CTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA	1567
Db	1501	CTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA	1560
QY	1568	AGGACTTACAGGGACAGCCGCGCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTTAG	1627
Db	1561	AGGACTTACAGGGACAGCCGCGCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTTAG	1620
QY	1628	CACAAAGGATGAGACACACGAAATGTATTTGCAAAATGTTCAAAATGCTTAACGGAGG	1687
Db	1621	CACAAAGGATGAGACACACGAAATGTATTTGCAAAATGTTCAAAATGCTTAACGGAGG	1680
QY	1688	CTGGTGGTTGATGATGTGTCCTTCCAACTTGACGGAATGTACTATCCACAGAGCA	1747
Db	1681	CTGGTGGTTGATGATGTGTCCTTCCAACTTGACGGAATGTACTATCCACAGAGCA	1740
QY	1748	GAACCAATAAAGTTCAACGGCATTAATGGTACTACTGGAAGGCTCAGGCTATTTCGCT	1807
Db	1741	GAACCAATAAAGTTCAACGGCATTAATGGTACTACTGGAAGGCTCAGGCTATTTCGCT	1800
QY	1808	GAAGGCCAACATGATGATCGGACGACGATTTCTAAACATCCAGTCCACCTGAGG	1867
Db	1801	GAAGGCCAACATGATGATCGGACGACGATTTCTAAACATCCAGTCCACCTGAGG	1860
QY	1868	AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACCTGAAAGTCACGGCTGCACA	1927
Db	1861	AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACCTGAAAGTCACGGCTGCACA	1920
QY	1928	CTGTGTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA	1987
Db	1921	CTGTGTCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA	1980
QY	1988	GATTAGAGCTGTAACTTTATCACTTAAACTTGATCACTTAAAGGACCAAGCAAGAC	2047
Db	1981	GATTAGAGCTGTAACTTTATCACTTAAACTTGATCACTTAAAGGACCAAGCAAGAC	2040
QY	2048	CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA	2107
Db	2041	CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA	2100
QY	2108	GAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAGAAATTTATGTGCAAGTTT	2167
Db	2101	GAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAGAAATTTATGTGCAAGTTT	2160
QY	2168	ATCAGTAATAACTGGAAAACAGAACATTTATGTTTATACAAATACAGATCATCTTGGAACT	2227
Db	2161	ATCAGTAATAACTGGAAAACAGAACATTTATGTTTATACAAATACAGATCATCTTGGAACT	2220
QY	2228	GCAATCTCTGAGCACTGTTTATACACTGTGTAATAATACCATATGTCTCT	2276
Db	2221	GCAATCTCTGAGCACTGTTTATACACTGTGTAATAATACCATATGTCTCT	2269

RESULT 7	
AAS70958	
ID	AAS70958 standard; cDNA; 2269 BP.
XX	
AC	AAS70958;
XX	
DT	13-FEB-2002 (first entry)
XX	
DE	DNA encoding novel human diagnostic protein #6762.
XX	
KW	Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
OS	Homo sapiens.
XX	
PN	WO200175067-A2.
PD	11-OCT-2001.
XX	
PF	30-MAR-2001; 2001WO-US008631.
PR	31-MAR-2000; 2000US-00540217.
XX	
PR	23-AUG-2000; 2000US-00649167.
XX	
PA	(HYSE-) HYSEQ INC.
XX	
PI	Drmanac RT, Liu C, Tang YT;
XX	
DR	WPI; 2001-639362/73.
DR	P-PSDB; ABG06771.
XX	
PT	New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
PT	
PT	
PT	
XX	
PS	Claim 1; SEQ ID NO 6762; 103pp; English.
XX	
CC	The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (III) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	
SQ	Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;
Query Match	99.4%; Score 2269; DB 5; Length 2269;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 2269; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
QY	8 TGGGTGGTGGTTATCTCCTCCAGCCTTGAGGGAGGAAACAACACTGTAGATCTGGGG 67
Db	1 TGGGTGGTGGTTATCTCCTCCAGCCTTGAGGGAGGAAACAACACTGTAGATCTGGGG 60
QY	68 AGAGGGAACAAGACCGCTGAAGCTCTCTGTAAAGCTGACACACCTCCCACTG 127

Db 61 AGAGAGAAACAAGGACCGTGAAAGCTGCTCTGTAAAGCTGACACAGCCCTCCCAAGTG 120
Qy 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTCTTACTGATGCTGAGAGAAACACAG 187
Db 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTCTTACTGATGCTGAGAGAAACACAG 180
Qy 188 CAGTAAACACAGGTTTGCTACTGGAAGAAAGAGAGAAAGAGACATTTCAATTGACCGACC 247
Db 181 CAGTAAACACAGGTTTGCTACTGGAAGAAAGAGAGAAAGAGACATTTCAATTGACCGACC 240
Qy 248 CAGCCATGGCAGCTAGCAGCCCTGGGTTTTCAGACGCGACAGCTCGGACCTCTGACAGCT 307
Db 241 CAGCCATGGCAGCTAGCAGCCCTGGGTTTTCAGACGCGACAGCTCGGACCTCTGACAGCT 300
Qy 308 GTGTTTGGCCCTCAAGTTTGTCTAAGCTGCTGTTTATTTACTGAAAGAAAGAAATGTGGCAGAT 367
Db 301 GTGTTTGGCCCTCAAGTTTGTCTAAGCTGCTGTTTATTTACTGAAAGAAAGAAATGTGGCAGAT 360
Qy 368 TGTGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGACGCTATAAACACTTTTCGGA 427
Db 361 TGTGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCGGACGCTATAAACACTTTTCGGA 420
Qy 428 GAGCATGGACAGCATAGGAAGAGCAATATCAGGTCAGCATGGGTCCCTGACAGCTACAC 487
Db 421 GAGCATGGACAGCATAGGAAGAGCAATATCAGGTCAGCATGGGTCCCTGACAGCTACAC 480
Qy 488 TTTCTCTCTCCAGAGATGACAACTGCCGCTCTTCTCCAGGCCCTTACGTGTCCTCAATGC 547
Db 481 TTTCTCTCTCCAGAGATGACAACTGCCGCTCTTCTCCAGGCCCTTACGTGTCCTCAATGC 540
Qy 548 TGTGCAAGAGGACCGCGCTCGAATACGATGATCTGGTGCAGAGGCTGCAAGTGTGGA 607
Db 541 TGTGCAAGAGGACCGCGCTCGAATACGATGATCTGGTGCAGAGGCTGCAAGTGTGGA 600
Qy 608 GAACATCATGGAACAACTCAGTGGCTTAATGACAGTCTGCAATTAATATCCAGGACAA 667
Db 601 GAACATCATGGAACAACTCAGTGGCTTAATGACAGTCTGCAATTAATATCCAGGACAA 660
Qy 668 CATGAGAAAGAAATGCTAGAGATACAGCAGATGCAAGATGCAAGAACAGAGCTGTGAT 727
Db 661 CATGAGAAAGAAATGCTAGAGATACAGCAGATGCAAGATGCAAGAACAGAGCTGTGAT 720
Qy 728 GATAGAAATAGGACAACTGTTGAAACCAACAGCTGAGCAAAACCGGGAAGTTAACTGA 787
Db 721 GATAGAAATAGGACAACTGTTGAAACCAACAGCTGAGCAAAACCGGGAAGTTAACTGA 780
Qy 788 TGTGGAAGCCCAAGTATTAATCAGACCAAGAGCTTGAACCTCAGCTCTTGGAACTC 847
Db 781 TGTGGAAGCCCAAGTATTAATCAGACCAAGAGCTTGAACCTCAGCTCTTGGAACTC 840
Qy 848 CCTCTCGACAAACAAATTTGGAACAAACAGATTTTGGACAGACCAAGTGAATTAACAAATTT 907
Db 841 CCTCTCGACAAACAAATTTGGAACAAACAGATTTTGGACAGACCAAGTGAATTAACAAATTT 900
Qy 908 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGAGTGTAGCTATGGAAGAACAGCAATCAT 967
Db 901 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGAGTGTAGCTATGGAAGAACAGCAATCAT 960
Qy 968 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCAGCAAAA 1027
Db 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCAGCAAAA 1020
Qy 1028 TTCCATCATTTGAAGAACTAGAAAAAATAAGTACCTGCCACGGTGAATTAATTCAGTTCT 1087
Db 1021 TTCCATCATTTGAAGAACTAGAAAAAATAAGTACCTGCCACGGTGAATTAATTCAGTTCT 1080
Qy 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAATAACTTACTGACTATGATGTCCAC 1147
Db 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAATAACTTACTGACTATGATGTCCAC 1140
Qy 1148 ATCAAACTCAGCTAAGGACCCCACTGTGCTTAAAGAGAGAAACAAATCAGCTTCAGAGACTG 1207
Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTGCTTAAAGAGAGAAACAAATCAGCTTCAGAGACTG 1200

Qy 1208 TGCTGAGTATTCAAAATCAGGACACACCAAAATGCGATCTACACGTTAAACATTCCCTAA 1267
Db 1201 TGCTGAGTATTCAAAATCAGGACACACCAAAATGCGATCTACACGTTAAACATTCCCTAA 1260
Qy 1268 TTCTACAGAAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGGGGGTGGCAAT 1327
Db 1261 TTCTACAGAAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGGGGGTGGCAAT 1320
Qy 1328 TATTACAGCACTGAGGATGGCAGCGTTGATTTTTCAGAGCACTTGAAGAAATATAAAGT 1387
Db 1321 TATTACAGCACTGAGGATGGCAGCGTTGATTTTTCAGAGCACTTGAAGAAATATAAAGT 1380
Qy 1388 GGGATTTGTTAAACCTTTCAGGAGAAATTTGGCTGGGAAATGATTTTTCGCAACTGAC 1447
Db 1381 GGGATTTGTTAAACCTTTCAGGAGAAATTTGGCTGGGAAATGATTTTTCGCAACTGAC 1440
Qy 1448 TAAATCAGCAACGCTATGCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1507
Db 1441 TAAATCAGCAACGCTATGCTTAAATAACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1500
Qy 1508 CTCATTGTATGAACATTTCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1567
Db 1501 CTCATTGTATGAACATTTCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1560
Qy 1568 AGGACTTACAGGACAGCGCGCAAAATAGCAGCATCAGCCACACGAGGAATGATTTAG 1627
Db 1561 AGGACTTACAGGACAGCGCGCAAAATAGCAGCATCAGCCACACGAGGAATGATTTAG 1620
Qy 1628 CACAAAGGATGGAGACAAACGACAAATGTTTTCAAATGTTTCAAAATGCTAAACAGGAGG 1687
Db 1621 CACAAAGGATGGAGACAAACGACAAATGTTTTCAAATGTTTTCAAATGCTAAACAGGAGG 1680
Qy 1688 CTGGTGGTTGATGATGTGCTTCCAACTTTGAAACGGAATGATCTATCCACAGAGGCA 1747
Db 1681 CTGGTGGTTGATGATGTGCTTCCAACTTTGAAACGGAATGATCTATCCACAGAGGCA 1740
Qy 1748 GAACACAAATTAAGTTCAAACGCGATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1807
Db 1741 GAACACAAATTAAGTTCAAACGCGATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1800
Qy 1808 CRAAGGCCAACCACTGATCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG 1867
Db 1801 CRAAGGCCAACCACTGATCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG 1860
Qy 1868 AACTGTCTCGAACTATTTTCAAAGACTTAAGCCCGAGTGCACTGAAAGTCAAGGCTGCGCA 1927
Db 1861 AACTGTCTCGAACTATTTTCAAAGACTTAAGCCCGAGTGCACTGAAAGTCAAGGCTGCGCA 1920
Qy 1928 CTGTGCTCTTCCACACAGAGGGCGTGTGCTGCTGCTGACCGGACCCACATGCTCCA 1987
Db 1921 CTGTGCTCTTCCACACAGAGGGCGTGTGCTGCTGCTGCTGACCGGACCCACATGCTCCA 1980
Qy 1988 GATTAGGCTCTGTAACCTTTTATCACTTAACTTGCATCACTTAAACGACCAAGCAAGAC 2047
Db 1981 GATTAGGCTCTGTAACCTTTTATCACTTAACTTGCATCACTTAAACGACCAAGCAAGAC 2040
Qy 2048 CCTAAACATCCATAATTTGATTTAGACAGAACACCTATGCAAGATGAAACCGGAGGCTGA 2107
Db 2041 CCTAAACATCCATAATTTGATTTAGACAGAACACCTATGCAAGATGAAACCGGAGGCTGA 2100
Qy 2108 GAATCAGACTGACAGTTTACAGCGCTGTGTCAACCAAGAAATGTTATGTGCAAGTTT 2167
Db 2101 GAATCAGACTGACAGTTTACAGCGCTGTGTCAACCAAGAAATGTTATGTGCAAGTTT 2160
Qy 2168 ATCAGTAAATTAATCGGAACACAGCACTTATGTTATACAAATCAGATCATCTTGGAACT 2227
Db 2161 ATCAGTAAATTAATCGGAACACAGCACTTATGTTATACAAATCAGATCATCTTGGAACT 2220
Qy 2228 GCATTTCTTCGAGCACTGTTTATACACTGTGTAATATACCATATGCTCT 2276
Db 2221 GCATTTCTTCGAGCACTGTTTATACACTGTGTAATATACCATATGCTCT 2269

RESULT 8
ABZ35349
ID ABZ35349 standard; cDNA; 2269 BP.
XX AC ABZ35349;
XX DT 05-FEB-2003 (first entry)
XX DE Human gene expression profile polynucleotide SEQ ID NO 460.
XX KW Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW gene expression; gene; ss.
XX OS Homo sapiens.
XX PN WO200274979-A2.
XX PD 26-SEP-2002.
XX PF 20-MAR-2002; 2002WO-US008456.
XX PR 20-MAR-2001; 2001US-0276947P.
XX PA (ORTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX PI Wan J, Wang Y;
XX WPI; 2002-740862/80.
XX New gene expression profile generated from primary, endothelial,
PT epithelial, and muscle cell types, useful for identifying disease
PT pathologies involving alterations of gene expression, e.g. cancer.
XX
PS Example 3; Page 609-610; 850pp; English.
XX
XX The invention relates to a gene expression profile comprising one or more
CC genes (ABZ3489-ABZ35692) and generated from a cell type. The cell type
CC is a coronary artery endothelium, umbilical artery or vein endothelium,
CC aortic endothelium, dermal microvascular endothelium, pulmonary artery
CC endothelium, myometrium microvascular endothelium, keratinocyte
CC epithelium, bronchial epithelium, mammary epithelium, prostate
CC epithelium, renal cortical epithelium, renal proximal tubule epithelium,
CC small airway epithelium, renal epithelium, umbilical artery smooth
CC muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
CC dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
CC aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
CC bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
CC osteoblasts or prostate stromal cell. The gene expression profile is used
CC for determining the level of RNA expression for a sample, determining the
CC phenotype of a cell and distinguishing cell types. The gene or a protein
CC expression profile is useful in identifying disease pathologies involving
CC alterations of gene expression. The assessment of expression profiles may
CC provide meaningful information with respect to tumour type and stage,
CC treatment methods, and prognosis. The gene or protein expression profile
CC may also be used for creating microarrays. The microarray is useful for
CC genetic and physical mapping of genomes, DNA sequencing, genetic or
CC medical diagnosis, genotyping of organisms, confirming cell or tissue
CC identifications and in identifying promising antibiotics, antiviral or
XX antifungal agents
SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;
Query Match 99.4%; Score 2269; DB 6; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 67
DB 1 TGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 60

QY 68 AGAGAGGAACAAGACCGTGAAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCCAAGTG 127
DB 61 AGAGAGGAACAAGACCGTGAAAGCTGCTCTGTAAAAAGCTGACACAGCCCTCCCAAGTG 120
QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAGAACACAG 187
DB 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAGAACACAG 180
QY 188 CAGTAAAAAACACAGGTTTCTACTGAAAAAGAGGAAAGAGAGACTTTTCATTGACGGACC 247
DB 181 CAGTAAAAAACACAGGTTTCTACTGAAAAAGAGGAAAGAGAGACTTTTCATTGACGGACC 240
QY 248 CAGCCATGCGCAGCTAGCAGCCCTCGGTTTCAGACGGCAGCAGCTCGGAGCTCTCGACGT 307
DB 241 CAGCCATGCGCAGCTAGCAGCCCTCGGTTTCAGACGGCAGCAGCTCGGAGCTCTCGACGT 300
QY 308 GTGTTTGGCCTCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAAGATGTGACAGAT 367
DB 301 GTGTTTGGCCTCAAGTTTGTCTAAGCTGCTGGTTTATTACTGAAGAAAGATGTGACAGAT 360
QY 368 TGTGTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAACCTTTCGGAA 427
DB 361 TGTGTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAACCTTTCGGAA 420
QY 428 GAGCATGGACGACATAGGAAAGAGCAATATCAGGTCCAGCATGGGTCTCGCAGCTACAC 487
DB 421 GAGCATGGACGACATAGGAAAGAGCAATATCAGGTCCAGCATGGGTCTCGCAGCTACAC 480
QY 488 TTTCTCTCTGCGAGATGGACACTGCGCTCTTCTCCAGCCCTACGTTGTCCTCAATGC 547
DB 481 TTTCTCTCTGCGAGATGGACACTGCGCTCTTCTCCAGCCCTACGTTGTCCTCAATGC 540
QY 548 TGTGAGAGGAGCGCGCTCGAATACGATACGCTCGGTGCGAGGCTGCAAGTCTCTGA 607
DB 541 TGTGAGAGGAGCGCGCTCGAATACGATACGCTCGGTGCGAGGCTGCAAGTCTCTGA 600
QY 608 GAACATCATGGAACAAACACTCTCAGTGGCTAATGAAGCTTGAGAAATATATCCAGGACAA 667
DB 601 GAACATCATGGAACAAACACTCTCAGTGGCTAATGAAGCTTGAGAAATATATCCAGGACAA 660
QY 668 CATGAAGAAGAAATGGTAGAGATACAGCAGAAATGCAGTACAGACACGAGCGGTGTGAT 727
DB 661 CATGAAGAAGAAATGGTAGAGATACAGCAGAAATGCAGTACAGACACGAGCGGTGTGAT 720
QY 728 GATAGAAATAGGGAACAAACCTGTTGAACCAACAGCTCAGCAAAACCGGGAAGTTAACTGA 787
DB 721 GATAGAAATAGGGAACAAACCTGTTGAACCAACAGCTCAGCAAAACCGGGAAGTTAACTGA 780
QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGCTTGAACCTTTCAGCTCTTGGAAACATC 847
DB 781 TGTGGAAGCCCAAGTATTAAATCAGACCAAGAGCTTGAACCTTTCAGCTCTTGGAAACATC 840
QY 848 CCTCTCGAACAACAAATTTGGAACCAAGAGTATTTGGACCAAGCCAGTGAATAAACAATTT 907
DB 841 CCTCTCGAACAACAAATTTGGAACCAAGAGTATTTGGACCAAGCCAGTGAATAAACAATTT 900
QY 908 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGTGTAGCTATGGAAGCAAGCAATCAT 967
DB 901 GCAAGATAAGAACAGTTTCTTAGAAAAAGAGTGTAGCTATGGAAGCAAGCAATCAT 960
QY 968 CCACTACAGTCAATATAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCAGCAACAAA 1027
DB 961 CCACTACAGTCAATATAAAGAGAGAAAGATCAGCTACAGGTGTAGTATCCAGCAACAAA 1020
QY 1028 TTCCATCATTTGAGAACTAGAAAAAATAATAGTCTGCCAGCGTGAATAATTCAGTTCT 1087
DB 1021 TTCCATCATTTGAGAACTAGAAAAAATAATAGTCTGCCAGCGTGAATAATTCAGTTCT 1080
QY 1088 TCAAAAGCAGCAACATGATCTCATGAGACAGATTAAATAACTTACTGACTATGATGTCAC 1147
DB 1081 TCAAAAGCAGCAACATGATCTCATGAGACAGATTAAATAACTTACTGACTATGATGTCAC 1140
QY 1148 ATCAAACTCAGTAAGGACCCCACTGTTGTTAAAGAGAAACAATCAGCTTCAGAGACTG 1207

Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGTTAAAGAAAGAACAAATCAGCTTCAGAGACTG 1200
Qy 1208 TGCTGAAGTATTCAAAATCAGGACACACCAAAATGCACTTACACCTTAACATTTCCCTTAA 1267
Db 1201 TGCTGAAGTATTCAAAATCAGGACACACCAAAATGCACTTACACCTTAACATTTCCCTTAA 1260
Qy 1268 TTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGACAAT 1327
Db 1261 TTCTACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGACAAT 1320
Qy 1328 TATTACAGCAGTGAAGATGCGAGCGCTGATTTTTCAGAGGACTTGAAGAGATATAAAGT 1387
Db 1321 TATTACAGCAGTGAAGATGCGAGCGCTGATTTTTCAGAGGACTTGAAGAGATATAAAGT 1380
Qy 1388 GGGATTGTTGTAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTGTTTCGCAACTGAC 1447
Db 1381 GGGATTGTTGTAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTGTTTCGCAACTGAC 1440
Qy 1448 TAATCAGCAACGCTATGTGCTTAAAAATACACCTTAAAGACTGGAAAGGGAATGAGGCTTA 1507
Db 1441 TAATCAGCAACGCTATGTGCTTAAAAATACACCTTAAAGACTGGAAAGGGAATGAGGCTTA 1500
Qy 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGATTACACCTTAA 1567
Db 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATATAGATTACACCTTAA 1560
Qy 1568 AGGACTTCAGGACACCGCGGCAAAATATAGCAGCATCAGCCACAGGAAATGATTTTAG 1627
Db 1561 AGGACTTCAGGACACCGCGGCAAAATATAGCAGCATCAGCCACAGGAAATGATTTTAG 1620
Qy 1628 CACAAAGGATGGAGACAAACACAAATGTTTTCAAATGTTTCAAAATGCTTAAACAGGAG 1687
Db 1621 CACAAAGGATGGAGACAAACACAAATGTTTTCAAATGTTTCAAAATGCTTAAACAGGAG 1680
Qy 1688 CTGGTGGTTGATGATGCTGCTTCCAACTTGAACGGGAATGTACTATCCACAGAGGCA 1747
Db 1681 CTGGTGGTTGATGATGCTGCTTCCAACTTGAACGGGAATGTACTATCCACAGAGGCA 1740
Qy 1748 GAACACAAATAGCTTCAAGGCAATTAATGCTACTGTAAGGCTCAGGCTATTCGCT 1807
Db 1741 GAACACAAATAGCTTCAAGGCAATTAATGCTACTGTAAGGCTCAGGCTATTCGCT 1800
Qy 1808 CAAGGACACCAACCATGATGATCGGACAGCAGATTTTCTAAACATCCAGTCCACCTGAGG 1867
Db 1801 CAAGGACACCAACCATGATGATCGGACAGCAGATTTTCTAAACATCCAGTCCACCTGAGG 1860
Qy 1868 AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCATGAAAGTCAAGGCTGCGCA 1927
Db 1861 AACTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCATGAAAGTCAAGGCTGCGCA 1920
Qy 1928 CTGTGCTCTTCCACACAGAGGGGCTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987
Db 1921 CTGTGCTCTTCCACACAGAGGGGCTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980
Qy 1988 GATTAGAGCTGTAAACCTTTATCATTTAAACTGTCATCACTTAACGAGCAACCAAGCAAGAC 2047
Db 1981 GATTAGAGCTGTAAACCTTTATCATTTAAACTGTCATCACTTAACGAGCAACCAAGCAAGAC 2040
Qy 2048 CCTAAACATCCATAATTTGATTAGACAGAACCTTATGCAAGATGAACCCGAGGCTGA 2107
Db 2041 CCTAAACATCCATAATTTGATTAGACAGAACCTTATGCAAGATGAACCCGAGGCTGA 2100
Qy 2108 GAATCAGACTGACAGTTTACAGAGCGTGTGTACACACCAAGATGTTATGTGCAAGTTT 2167
Db 2101 GAATCAGACTGACAGTTTACAGAGCGTGTGTACACACCAAGATGTTATGTGCAAGTTT 2160
Qy 2168 ATCAGTAAATACCTGGAAGAAACAGAACTTATGTTATACAAATACAGATCATCTTGGAACT 2227
Db 2161 ATCAGTAAATACCTGGAAGAAACAGAACTTATGTTATACAAATACAGATCATCTTGGAACT 2220
Qy 2228 GCATTCTTCTGAGCAGCTGTTTATACACTGTGTTAAATACCCATATGTCCT 2276

Db 2221 GCATTCTTCTGAGCAGCTGTTTATACACTGTGTAAATACCCATATGTCCT 2269
RESULT 9
ABK47716
ID ABK47716 standard; DNA; -2269 BP.
XX ABK47716;
AC ABK47716;
XX DT 02-JUL-2002 (first entry)
XX DNA encoding human angiopoietin-2.
DE Human; immunoconjugate; anti-vascular endothelial growth factor antibody;
KW anti-VEGF antibody; monoclonal antibody 2C3 ATCC PTA 1595; VEGF receptor;
KW VEGFR2; KDR/Flk-1; VEGFR1; Flt-1; angiogenesis; macular degeneration;
KW ocular neovascular disease; cancer; vascularised solid tumour; AIDS;
KW metastatic tumour; endothelial cell proliferation; inflammatory disorder;
KW atherosclerosis; diabetic retinopathy; corneal graft rejection;
KW acquired immune deficiency syndrome; infection; restenosis; fungal ulcer;
KW sickle cell anaemia; endometriosis; angiopoietin-2; gene; ds.
XX Homo sapiens.
OS
Key Location/Qualifiers
CDS 350..1840
FT /*tag= a
FT /product= "Angiopoietin-2"
XX AU200179401-A.
XX 06-DEC-2001.
XX 12-OCT-2001; 2001AU-00079401.
XX 28-APR-2000; 2000AU-00048049.
XX (TEXA) UNIV TEXAS SYSTEM.
XX Thorpe PE, Brekken RA;
XX WPI; 2002-281368/33.
XX P-PSDB; AAU77944.
XX Immunoconjugate compositions for treating cancer by inhibiting
PT angiogenesis and for delivering a diagnostic agent to tumor, comprises
PT anti-vascular endothelial growth factor antibody attached to a biological
PT agent.
XX Disclosure; Page 4 (Sequence listing); 299pp; English.
PS The present invention relates to antibody-based compositions comprising
CC an immunoconjugate such as anti-vascular endothelial growth factor (VEGF)
CC antibody (Ab) (or its antigen-binding fragment), attached to a biological
CC agent, where the Ab binds to the same epitope as the monoclonal antibody
CC (Mab) 2C3 ATCC PTA 1595, and significantly inhibits VEGF binding to the
CC VEGF receptor (KDR/Flk-1) without inhibiting VEGF binding to the
CC VEGF receptor VEGFR1 (Flt-1). The compositions of the invention are
CC useful in therapy, and diagnosis, for inhibiting angiogenesis in an
CC animal having ocular neovascular disease or macular degeneration, and for
CC delivering a biological agent to a vascularised tumour. The compositions
CC can also be used for treating cancer and subjects at risk of developing,
CC a vascularised solid tumour, a metastatic tumour or metastases from a
CC primary tumour. The composition is useful for specifically inhibiting
CC VEGF-induced endothelial cell proliferation, without significantly
CC inhibiting VEGF-induced macrophage, osteoclast or chondroblast function.
CC The compositions can be used for treating various diseases such as
CC inflammatory disorders, atherosclerosis, diabetic retinopathy,
CC restenosis, acquired immune deficiency syndrome (AIDS), blood borne
CC tumours, corneal graft rejection, Crohn's disease, fungal ulcers,
CC infections, sickle cell anaemia, and endometriosis. The present sequence
CC encodes human angiopoietin-2. Angiopoietin-2 may be attached or
CC functionally associated with anti-VEGF antibodies

XX	Sequence	2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;	
SQ	Query Match	99.4%; Score 2269; DB 6; Length 2269;	
	Best Local Similarity	100.0%; Pred. No. 0;	
	Matches 2269; Conservative	0; Mismatches 0; Indels 0; Gaps 0;	
QY	8	TGGGTGGTGTATCTCTCCAGCCTTTGAGGGAGGAAACAACACTGTAGGATCTGGGG	67
DB	1	TGGGTGGTGTATCTCTCCAGCCTTTGAGGGAGGAAACAACACTGTAGGATCTGGGG	60
QY	68	AGAGAGAAACAAGACCGTGAAAGTGTCTCTGTAAGAGCTGACACAGCCCTCCCAAGTG	127
DB	61	AGAGAGAAACAAGAGCCGTGAAAGTGTCTCTGTAAGAGCTGACACAGCCCTCCCAAGTG	120
QY	128	ACGAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTTGCAATGCTGCGAGAGAACACAG	187
DB	121	ACGAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTTGCAATGCTGCGAGAGAACACAG	180
QY	188	CAGTAAAAACCAAGTTTGCTACTGGAAAAAGAGGAAAGAGACTTTTCATTGACGGACC	247
DB	181	CAGTAAAAACCAAGTTTGCTACTGGAATAAGAGGAAAGAGAGACTTTTCATTGACGGACC	240
QY	248	CAGCCATGGCAGCTAGCAGCCCTGGGTTTACAGCGGAGAGCTCGGACTCTCGAAGT	307
DB	241	CAGCCATGGCAGCTAGCAGCCCTGGGTTTACAGCGGAGAGCTCGGACTCTCGAAGT	300
QY	308	GTGTTTGCCCTCAAGTTTGTCTAAGCTGCTGCTGTTTATTACTGAAGAAAGAAATGTGCAGAT	367
DB	301	GTGTTTGCCCTCAAGTTTGTCTAAGCTGCTGCTGTTTATTACTGAAGAAAGAAATGTGCAGAT	360
QY	368	TGTTTTCTTTACTCTGAGCTGTGATCTTGTCTTGCGCGCAGCCTATAACAATCTTCGGAA	427
DB	361	TGTTTTCTTTACTCTGAGCTGTGATCTTGTCTTGCGCGCAGCCTATAACAATCTTCGGAA	420
QY	428	GAGCATGAGCATAGAGAAAGAACATATCAGGTCTCAGATGAGGTCTGCGACTACAC	487
DB	421	GAGCATGAGCATAGAGAAAGAACATATCAGGTCTCAGATGAGGTCTGCGACTACAC	480
QY	488	TTTCTCTCTGCAGAGATGGAACAATGCGCGCTCTTCTTCCAGCCCTACGTCCTCAATGC	547
DB	481	TTTCTCTCTGCAGAGATGGAACAATGCGCGCTCTTCTTCCAGCCCTACGTCCTCAATGC	540
QY	548	TGTGAGAGGGACGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTGCAAGTCTGGA	607
DB	541	TGTGAGAGGGACGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTGCAAGTCTGGA	600
QY	608	GAAATCATGGAAGAAACAACACTCAGTGGCTATGAGCTTGAGATTTATATCCAGACAA	667
DB	601	GAAATCATGGAAGAAACAACACTCAGTGGCTATGAGCTTGAGATTTATATCCAGACAA	660
QY	668	CATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT	727
DB	661	CATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAGTACAGAACCCAGCGCTGTGAT	720
QY	728	GATAGAAATAGGACAAACCTGTGAAACCAACAGCTGAGCAAAACCGGAAAGTTAACTGA	787
DB	721	GATAGAAATAGGACAAACCTGTGAAACCAACAGCTGAGCAAAACCGGAAAGTTAACTGA	780
QY	788	TGTGAAGCCCAAGTATTTAAATCAGACACAGACTTGAACTTTCAGCTCTTGGAACAATC	847
DB	781	TGTGAAGCCCAAGTATTTAAATCAGACACAGACTTGAACTTTCAGCTCTTGGAACAATC	840
QY	848	CCTCTCGACAAACAATTTGGAAGAAACAGATTTTGGACAGACAGCTGAAATTAACAATTT	907
DB	841	CCTCTCGACAAACAATTTGGAAGAAACAGATTTTGGACAGACAGCTGAAATTAACAATTT	900
QY	908	GCAAGATAAGAACAGTTTCTAGAAAAAGAGGTGTCTAGCTATGGAAGACAGACATCAT	967
DB	901	GCAAGATAAGAACAGTTTCTAGAAAAAGAGGTGTCTAGCTATGGAAGACAGACATCAT	960
QY	968	CCAACTACGTCAATAAAGAGAGAGATCAGCTACAGGTGTAGTATCCAAAGCAAAA	1027
DB			
961	CCAACTACAGTCAATAAAGAGAGAGATCAGCTACAGGTGTAGTATCCAAAGCAAAA	1020	
1028	TTCCCATTTGAAGAACTAGAAAAAAAATAGTACTGCGACGGTGAATAATTCAGTTCT	1087	
1021	TTCCCATTTGAAGAACTAGAAAAAAAATAGTACTGCGACGGTGAATAATTCAGTTCT	1080	
1088	TCAAAAGCAGCAACAATGATCTCATGAGACAGTCTAATTAACCTTACGATGATGTCAC	1147	
1081	TCAAAAGCAGCAACAATGATCTCATGAGACAGTCTAATTAACCTTACGATGATGTCAC	1140	
1148	ATCAAACTCAGTAAAGACCCCACTGTTCTTAAAGAGAACAAATCAGCTTCAGAGACTG	1207	
1141	ATCAAACTCAGTAAAGACCCCACTGTTCTTAAAGAGAACAAATCAGCTTCAGAGACTG	1200	
1208	TGCTGAAGTATTCAAACTCAGGACACACCAAAATGGCATCTACAGTTAAACATTCCTAA	1267	
1201	TGCTGAAGTATTCAAACTCAGGACACACCAAAATGGCATCTACAGTTAAACATTCCTAA	1260	
1268	TTCTACAGAAAGAGATCAAGGGCTACTGTGACATGGAAGCTGGAGAGCGGGTGACAAAT	1327	
1261	TTCTACAGAAAGAGATCAAGGGCTACTGTGACATGGAAGCTGGAGAGCGGGTGACAAAT	1320	
1328	TATTCAGCGAGCTGAGGATGGCGGTTGATTTTCAGAGGACTTCGGAAGATATAAAGT	1387	
1321	TATTCAGCGAGCTGAGGATGGCGGTTGATTTTCAGAGGACTTCGGAAGATATAAAGT	1380	
1388	GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTTTCGCAACTGCAC	1447	
1381	GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAAATGAGTTTTCGCAACTGCAC	1440	
1448	TAATCAGCAACGCTATGCTTTAAATAACA CTTTAAAGACTGGGAAGGAATGAGGCTTA	1507	
1441	TAATCAGCAACGCTATGCTTTAAATAACA CTTTAAAGACTGGGAAGGAATGAGGCTTA	1500	
1508	CTCATTGTATGAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA	1567	
1501	CTCATTGTATGAACATTTCTATCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA	1560	
1568	AGGACTTACAGGGACAGCGCGCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTAG	1627	
1561	AGGACTTACAGGGACAGCGCGCAAAATAAGCAGCATCAGCCAAACAGGAAATGATTTAG	1620	
1628	CACAAAGATGGAGAACAGCAAAATGATTTTGCATAATGTTTCAAAATGCTTAAAGAGG	1687	
1621	CACAAAGATGGAGAACAGCAAAATGATTTTGCATAATGTTTCAAAATGCTTAAAGAGG	1680	
1688	CTGGTGTGTTGATGATGCTGCTTCCAACTTGAACCGAAATGTACTTCCACAGAGCA	1747	
1681	CTGGTGTGTTGATGATGCTGCTTCCAACTTGAACCGAAATGTACTTCCACAGAGCA	1740	
1748	GAAACAAATAGTTTCAACGGCATTTAAATGGTACTTACTGGAAAGGCTCAGGCTATTCGCT	1807	
1741	GAAACAAATAGTTTCAACGGCATTTAAATGGTACTTACTGGAAAGGCTCAGGCTATTCGCT	1800	
1808	CAAGGCCAACCAATGATGATCCGACCGAGATTTTCTAAACATCCCGATCCACCTGAGG	1867	
1801	CAAGGCCAACCAATGATGATCCGACCGAGATTTTCTAAACATCCCGATCCACCTGAGG	1860	
1868	AATGTCTCGAAGTATTTTCAAGACTTTAAAGCCAGTGCATCTGAAAGTCAAGGCTTCGCA	1927	
1861	AATGTCTCGAAGTATTTTCAAGACTTTAAAGCCAGTGCATCTGAAAGTCAAGGCTTCGCA	1920	
1928	CTGTGCTCTTCCACCAAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATCTCTCA	1987	
1921	CTGTGCTCTTCCACCAAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATCTCTCA	1980	
1988	GATTAGAGCCTGTAACTTTTACTTAAATCTTGATCACTTTAAACGGACCCAAAGCAAGAC	2047	
1981	GATTAGAGCCTGTAACTTTTACTTAAATCTTGATCACTTTAAACGGACCCAAAGCAAGAC	2040	
2048	CCTAAACATCCATTTGTTGATAGACAGACACCTATGCAAGATGAACCGGCTGCA	2107	
2041	CCTAAACATCCATTTGTTGATAGACAGACACCTATGCAAGATGAACCGGCTGCA	2100	

QY 968 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAA 1027
Db |||||
QY 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAA 1020
Db |||||
QY 1028 TTCCATCATTTGAAGAACTAGAAAAAATAAGTAGTACTGCCACGGTGAATAATTCAGTTCT 1087
Db |||||
QY 1021 TTCCATCATTTGAAGAACTAGAAAAAATAAGTAGTACTGCCACGGTGAATAATTCAGTTCT 1080
Db |||||
QY 1088 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTTACTGACTATCATGTCCAC 1147
Db |||||
QY 1081 TCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTTACTGACTATCATGTCCAC 1140
Db |||||
QY 1148 ATCAAACCTCAGCTAAGGACCCCACTGTTGCTTAAAGAAAGCAAAATCAGCTTCAGAGACTG 1207
Db |||||
QY 1141 ATCAAACCTCAGCTAAGGACCCCACTGTTGCTTAAAGAAAGCAAAATCAGCTTCAGAGACTG 1200
Db |||||
QY 1208 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCTTAA 1267
Db |||||
QY 1201 TGCTGAAGTATTCAAATCAGGACACACCAAAATGGCATCTACAGTTTAACTTCCTTAA 1260
Db |||||
QY 1268 TTCTCAGAAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGAGGGCGGTGGACAAT 1327
Db |||||
QY 1261 TTCTCAGAAAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGAGGGCGGTGGACAAT 1320
Db |||||
QY 1328 TATTTCAGGACGCTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAATATAAAGT 1387
Db |||||
QY 1321 TATTTCAGGACGCTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAATATAAAGT 1380
Db |||||
QY 1388 GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAATGATTTGTTCCCACTGAC 1447
Db |||||
QY 1381 GGGATTTGGTAAACCTTCAGGAGAAATATGGCTGGGAATGATTTGTTCCCACTGAC 1440
Db |||||
QY 1448 TAATCAGCAACGCTATGCTTTAAATAACACCTTAAAGACTGGGAAGGAATGAGGCTTA 1507
Db |||||
QY 1441 TAATCAGCAACGCTATGCTTTAAATAACACCTTAAAGACTGGGAAGGAATGAGGCTTA 1500
Db |||||
QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567
Db |||||
QY 1501 CTCATTGTATGAACATTTCTATCTCTCAAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560
Db |||||
QY 1568 AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTAG 1627
Db |||||
QY 1561 AGGACTTACAGGACAGCCGGCAAAATAGCAGCATCAGCCAAACAGGAAATGATTTAG 1620
Db |||||
QY 1628 CACAAAGGATGAGACAAACGACAAATGTATTTGCAAAATGTTCAAAATGCTTAAACAGGAGG 1687
Db |||||
QY 1621 CACAAAGGATGAGACAAACGACAAATGTATTTGCAAAATGTTCAAAATGCTTAAACAGGAGG 1680
Db |||||
QY 1688 CTGGTGGTTTGATGATGGTCTTCCAACTTGGAACCGGAATGTACTATCCACAGAGCA 1747
Db |||||
QY 1681 CTGGTGGTTTGATGATGGTCTTCCAACTTGGAACCGGAATGTACTATCCACAGAGCA 1740
Db |||||
QY 1748 GAACACAAATAGTTCAACGGCATTAATGGTACTACTGGAAAGGCTCAGGCTATTCGCT 1807
Db |||||
QY 1741 GAACACAAATAGTTCAACGGCATTAATGGTACTACTGGAAAGGCTCAGGCTATTCGCT 1800
Db |||||
QY 1808 CAAGGCCAACCATGATCATCCGACGACGATTTCTAAACATCCCACTGCAACCTGAGG 1867
Db |||||
QY 1801 CAAGGCCAACCATGATCATCCGACGACGATTTCTTAAACATCCCACTGCAACCTGAGG 1860
Db |||||
QY 1868 AACTGTCTCGAACTATTTTCAAAGACTTAAGCCCACTGCACTGAAAGTCAACGGCTGCGCA 1927
Db |||||
QY 1861 AACTGTCTCGAACTATTTTCAAAGACTTAAGCCCACTGCACTGAAAGTCAACGGCTGCGCA 1920
Db |||||
QY 1928 CTGTGCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987
Db |||||
QY 1921 CTGTGCTCTTCCACACAGAGGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980
Db |||||
QY 1988 GATTAGAGCCTGTAAACTTTTATCACTTAACTTTGATCACTTAAAGGACCAAGCAAGAC 2047
Db |||||
QY 1981 GATTAGAGCCTGTAAACTTTTATCACTTAACTTTGATCACTTAAAGGACCAAGCAAGAC 2040
Db |||||

QY 2048 CCTAAACATCCATTAATGTTGATTAGACAGAACACCTATGCAAAAGATGAACCCGAGCTGA 2107
Db |||||
QY 2041 CCTAAACATCCATTAATGTTGATTAGACAGAACACCTATGCAAAAGATGAACCCGAGCTGA 2100
Db |||||
QY 2108 GAATCAGACTGACAGTCTTACAGACGCTGCTGTCAACAACCAAGAAATGTTATGTGCAAGTTT 2167
Db |||||
QY 2101 GAATCAGACTGACAGTCTTACAGACGCTGCTGTCAACAACCAAGAAATGTTATGTGCAAGTTT 2160
Db |||||
QY 2168 ATCAGTAAATAACTCGAAAAACAGAACACTTATGTTTATACAATACAGATCATCTTGGAACT 2227
Db |||||
QY 2161 ATCAGTAAATAACTCGAAAAACAGAACACTTATGTTTATACAATACAGATCATCTTGGAACT 2220
Db |||||
QY 2228 GCATTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2276
Db |||||
QY 2221 GCATTTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCT 2269
Db |||||

RESULT 11
ADN95380

ID ADN95380 standard; DNA; 2269 BP.

XX AC ADN95380;

XX DT 01-JUL-2004 (first entry)

XX Human BEC/LEC-related gene sequence SeqID303.

DE growth; differentiation; blood endothelial cell; BEC;

XX lymphatic endothelial cell; LEC; hereditary lymphoedema; VEGFR-3;

KW lymphatic growth agent; VEGF-C; VEGF-D; antiangiogenic; cytostatic;

KW vasotropic; antiinflammatory; gene therapy; endothelial cell disorder;

KW inflammatory disease; cancer metastasis; lymphatic system; gene; ds;

KW human.

XX Homo sapiens.

OS WO2003080640-A1.

XX PD 02-OCT-2003.

XX PF 07-MAR-2003; 2003WO-US006900.

XX PR 07-MAR-2002; 2002US-0363019P.

XX PA (LUDW-) LUDWIG INST CANCER RES.

XX PI (LICN) LICENTIA LTD.

XX PI Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;

XX DR WPI; 2003-876999/81.

XX DR P-PSDB; ADN95379.

XX PS Example 1; SEQ ID NO 303; 176pp; English.

XX This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic endothelial cells (LEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises identifying a human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation correlates with lymphoedema in human subjects, and with the proviso that the LEC protein is not VEGFR-3; and administering to the subject a composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polynucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytostatic, vasotropic or antiinflammatory activity or for gene therapy. The method is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating hereditary lymphoedema, in screening for an endothelial cell disorder or predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the differential modulation of blood vessel endothelial

cell or lymphatic vessel endothelial cell growth or differentiation. The lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation in a LEC gene or of other diseases involving the lymphatic vessels, such as various inflammatory diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially expressed gene which is related to the method of the invention. Note: This sequence does not appear in the specification but was obtained by the CC indexer using the source data given in table 14 of the specification.

XX

SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;

Query Match 99.4%; Score 2269; DB 11; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGTGGTGTCTTATCTCTCCAGCCTTCAGGAGGGAACAACACTGTAGGATCTGGGG 67
DB 1 TGGTGGTGTCTTATCTCTCCAGCCTTCAGGAGGGAACAACACTGTAGGATCTGGGG 60

QY 68 AGAGAGGAAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACAGCCCTCCCAAGTG 127
DB 61 AGAGAGGAAACAAAGGACCGTGAAGCTGCTCTGTAAAGCTGACAGCCCTCCCAAGTG 120

QY 128 AGAGAGACTGTTCTTCCACTGCAATCTGACAGTTTACTTCATGCTGGAGAGAACACAG 187
DB 121 AGCAGGACTGTTCTTCCACTGCAATCTGACAGTTTACTTCATGCTGGAGAGAACACAG 180

QY 188 CAGTAAACACAGTTTGTCTGAAAGAGGAAAGAGAAAGAGTTCATTGACGAGAC 247
DB 181 CAGTAAACACAGTTTGTCTGAAAGAGGAAAGAGAAAGAGTTCATTGACGAGAC 240

QY 248 CAGCCATGGCAGGCTAGCAGCCCTGCGTTTTCAGACGCGCAGCTCGGACCTCTGACGCT 307
DB 241 CAGCCATGGCAGGCTAGCAGCCCTGCGTTTTCAGACGCGCAGCTCGGACCTCTGACGCT 300

QY 308 GTGTTTGGCCCTCAAGTTTGTAGCTGCTGCTGTTTATCTGAGAGAAAGATGTGGCAGAT 367
DB 301 GTGTTTGGCCCTCAAGTTTGTAGCTGCTGCTGTTTATCTGAGAGAAAGATGTGGCAGAT 360

QY 368 TGTGTTCTTCTTACTGAGCTGCTGATCTTGTCTGGCGCAGCCTATAAACAACTTTCGAA 427
DB 361 TGTGTTCTTCTTACTGAGCTGCTGATCTTGTCTGGCGCAGCCTATAAACAACTTTCGAA 420

QY 428 GAGCATGGACGATAGGAAGCAATATCAGGTCAGCAGCTGGGTCCTGCGACTACAC 487
DB 421 GAGCATGGACGATAGGAAGCAATATCAGGTCAGCAGCTGGGTCCTGCGACTACAC 480

QY 488 TTTCTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTTACGTTGCCAATGC 547
DB 481 TTTCTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTTACGTTGCCAATGC 540

QY 548 TGTGAGAGGAGCGCGCTCGAATACGATGCTCGGTCGAGGCTGCAAGTGTGGA 607
DB 541 TGTGAGAGGAGCGCGCTCGAATACGATGCTCGGTCGAGGCTGCAAGTGTGGA 600

QY 608 GAAATCATGGAACAACTCAGTGGCTTAATGAAGCTTGAGATTAATATCCAGGACAA 667
DB 601 GAAATCATGGAACAACTCAGTGGCTTAATGAAGCTTGAGATTAATATCCAGGACAA 660

QY 668 CATGAAGAAAGAAATGTGATGATACAGAGAAATGCAAGTACAGAACAGACGCTGTGAT 727
DB 661 CATGAAGAAAGAAATGTGATGATACAGAGAAATGCAAGTACAGAACAGACGCTGTGAT 720

QY 728 GATGAATAATAGGACAACTGTTGAACCAACAGCTGACCAACCGGAGTTAACTGA 787
DB 721 GATGAATAATAGGACAACTGTTGAACCAACAGCTGACCAACCGGAGTTAACTGA 780

QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCAAGACTTTGAACTTCAGTCTTTGGAACACTC 847
DB 781 TGTGGAAGCCCAAGTATTAAATCAGACCAAGACTTTGAACTTCAGTCTTTGGAACACTC 840

QY 848 CCTCTCGACAAACAAATTTGGAAACACAGATTTTGGACCGACAGTGAATAAACAATTT 907

DB 841 CCTCTCGACAAACAAATTTGGAAACACAGATTTTGGACCGACAGCCAGTGAATAACAATTT 900
QY 908 GCAAGATAAGAACAGTTTCTAGAAAAGAGTGCTAGCTATGGAAGACAGACATCAT 967
DB 901 GCAAGATAAGAACAGTTTCTAGAAAAGAGTGCTAGCTATGGAAGACAGACATCAT 960

QY 968 CCACTACTAGTCAATAAAGAGAGAGAAAGTACAGCTACAGGTGTTAGTATCCCAAGCAAAA 1027
DB 961 CCACTACTAGTCAATAAAGAGAGAGAAAGTACAGCTACAGGTGTTAGTATCCCAAGCAAAA 1020

QY 1028 TTCCATCATTTGAAGAACTAGAAAAAATAATAGTGACTGCCACCGTGAATAATTTAGTTCT 1087
DB 1021 TTCCATCATTTGAAGAACTAGAAAAAATAATAGTGACTGCCACCGTGAATAATTTAGTTCT 1080

QY 1088 TCAAAAGCAGCAACATGATCTCATGAGACAGTTTAATACTTACTGACTATGATGTCAC 1147
DB 1081 TCAAAAGCAGCAACATGATCTCATGAGACAGTTTAATACTTACTGACTATGATGTCAC 1140

QY 1148 ATCAAACTCAGCTTAAGGACCCCACTGTTGCTTAAAGAGAACAAATCAGCTTTCAGAGACTG 1207
DB 1141 ATCAAACTCAGCTTAAGGACCCCACTGTTGCTTAAAGAGAACAAATCAGCTTTCAGAGACTG 1200

QY 1208 TGTGAAGTATTCAAATCAGGACACACCAAAATGCGATCTACACGTTTAACTTCCCTAA 1267
DB 1201 TGTGAAGTATTCAAATCAGGACACACCAAAATGCGATCTACACGTTTAACTTCCCTAA 1260

QY 1268 TTCTCAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGGACAAT 1327
DB 1261 TTCTCAGAGAGATCAAGGCCCTACTGTGACATGGAAGCTGGAGAGCGGGTGGACAAT 1320

QY 1328 TATTACGCGAGCTGAGGATGGAGCGTTGATTTTTCAGAGACTTGGAAAGAAATATAAGT 1387
DB 1321 TATTACGCGAGCTGAGGATGGAGCGTTGATTTTTCAGAGACTTGGAAAGAAATATAAGT 1380

QY 1388 GGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAAATGAGTTTTCGCAACTGAC 1447
DB 1381 GGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAAATGAGTTTTCGCAACTGAC 1440

QY 1448 TAATCAGCAACGCTATGTCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA 1507
DB 1441 TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGGAAGGGAATGAGGCTTA 1500

QY 1508 CTCAATGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1567
DB 1501 CTCAATGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATATATAGGATTCACCTTAA 1560

QY 1568 AGGACTTACAGGACAGCGCGCAAAATAAGCAGCATCAGCCAAACCCAGGAAATGATTTAG 1627
DB 1561 AGGACTTACAGGACAGCGCGCAAAATAAGCAGCATCAGCCAAACCCAGGAAATGATTTAG 1620

QY 1628 CACAAAGGATGGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTACAGGAG 1687
DB 1621 CACAAAGGATGGAGACAAACGACAAATGTATTTGCAAAATGTTTCAAAATGCTTACAGGAG 1680

QY 1688 CTGGTGGTTTGTATGATGTGCTCTTCCAACTTGAACCGGAAATGTACTATCCAGAGGCA 1747
DB 1681 CTGGTGGTTTGTATGATGTGCTCTTCCAACTTGAACCGGAAATGTACTATCCAGAGGCA 1740

QY 1748 GAACACAAATAAGCTTCAACGGCATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1807
DB 1741 GAACACAAATAAGCTTCAACGGCATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1800

QY 1808 CAAGGCCCAACCAATGATGATCCGACAGAGATTTCTAAACATCCAGTCCACCTGAGG 1867
DB 1801 CAAGGCCCAACCAATGATGATCCGACAGAGATTTCTAAACATCCAGTCCACCTGAGG 1860

QY 1868 AACTGTCTGAACTATTTTCAAGACTTAAGCCAGTGCACTGAAAGTCAAGGCTGCGCA 1927
DB 1861 AACTGTCTGAACTATTTTCAAGACTTAAGCCAGTGCACTGAAAGTCAAGGCTGCGCA 1920

QY 1928 CTGTGTCTCTTCCACCAAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987

Db 1921 CTGTGTCCTCTCCACCACAGAGGGCGTGTGCTCGGTGTGACGGGACCCACATGCTCCA 1980
QY 1988 GATTAGAGCTGTAAACTTTATCACCTTAAACTTTGATCACTTAAACGGACCAAGCAAGAC 2047
Db 1981 GATTAGAGCTGTAAACTTTATCACCTTAAACTTTGATCACTTAAACGGACCAAGCAAGAC 2040
QY 2048 CCTAAACATCCATAATTTGATTAGACAGAACACCTTATCAAGATGAACCCGAGCTGA 2107
Db 2041 CCTAAACATCCATAATTTGATTAGACAGAACACCTTATCAAGATGAACCCGAGCTGA 2100
QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGCACAAACCAAGATGTTATGTCAGTTT 2167
Db 2101 GAATCAGACTGACAGTTTACAGACGCTGCTGCACAAACCAAGATGTTATGTCAGTTT 2160
QY 2168 ATCAGTAAATAACTGTAACCAAGAACACCTTATGTTTATACAAATACAGATCATCTTGAAC 2227
Db 2161 ATCAGTAAATAACTGTAACCAAGAACACCTTATGTTTATACAAATACAGATCATCTTGAAC 2220
QY 2228 GCATTCCTCTGAGCACTGTTTATACACTGTGTAAATATACCCATATGTCCT 2276
Db 2221 GCATTCCTCTGAGCACTGTTTATACACTGTGTAAATATACCCATATGTCCT 2269

RESULT 12
ADO28674
ID ADO28674 standard; cDNA; 2269 BP.
XX
AC ADO28674;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human Tie2 ligand2 encoding cDNA SEQ ID NO:103.
XX
KW high-grade dysplasia; HGD; oesophageal adenocarcinoma;
KW neo-plastic transformation; cancer; cytostatic; gene therapy; human;
KW Tie2 ligand2; chromosome 8; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 350..1840
FT /*tag= a
FT /*product= "Tie2 ligand2"
XX
PN WO2004044178-A2.
XX
PD 27-MAY-2004.
XX
PF 13-NOV-2003; 2003WO-US036260.
XX
PR 13-NOV-2002; 2002US-0425813P.
XX (GETH) GENENTECH INC.
XX
XX Smith V;
PI
XX WPI; 2004-420319/39.
DR P-PSDB; ADO28675.
XX
PT Detecting of high-grade dysplasia in cells of a mammalian tissue sample
PT comprises establishing the level of expression in the test tissue sample
PT of the genes.
XX
XX Claim 37; SEQ ID NO 103; 256pp; English.
XX
XX The present invention describes a method for detecting high-grade
XX dysplasia (HGD) in cells of a mammalian tissue sample. Also described:
XX (1) identifying an oesophageal tissue susceptible to oesophageal
XX adenocarcinoma; (2) determining the predisposition of a mammalian tissue
XX to a neo-plastic transformation by detecting HGD in cells of the tissue;
XX and (3) detecting cancer in a patient. The method can be used in
XX detecting HGD and cancer in cells of a mammalian tissue sample. The
XX methods and compositions of the present invention can be used in treating

CC and preventing HGD and cancer, and in gene therapy. The present sequence
CC encodes human Tie2 ligand2, which is used in the exemplification of the
CC present invention. The human Tie2 ligand2 gene is located on chromosome
XX 8.
SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;
Query Match 99.4%; Score 2269; DB 12; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TGGGTTGGTGTATTATCTCTCCAGCCTTGGAGGAGGGAACAACTGTAGATCTGGGG 67
Db 1 TGGGTTGGTGTATTATCTCTCCAGCCTTGGAGGAGGGAACAACTGTAGATCTGGGG 60
QY 68 AGAGAGGAACAAGACCGTGAAGCTGCTGTGTAAGAGCTGACACAGCCCTCCCAAGTG 127
Db 61 AGAGAGGAACAAGACCGTGAAGCTGCTGTGTAAGAGCTGACACAGCCCTCCCAAGTG 120
QY 128 AGCAGGACTGTTCTTTCCCACTGCAATCTGACAGTTTACTTGCAATGCTGAGAGAAACACAG 187
Db 121 AGCAGGACTGTTCTTTCCCACTGCAATCTGACAGTTTACTTGCAATGCTGAGAGAAACACAG 180
QY 188 CAGTAAAAACAGGTTTGTCTACTGSAAGAAAGAGGAAGAGACTTTTCATTGACGGACC 247
Db 181 CAGTAAAAACAGGTTTGTCTACTGSAAGAAAGAGGAAGAGACTTTTCATTGACGGACC 240
QY 248 CAGCCATGGCAGCTAGCAGCCCTCGGTTTTCAGACGGCAGCAGCTCGGACCTCTGGACGT 307
Db 241 CAGCCATGGCAGCTAGCAGCCCTCGGTTTTCAGACGGCAGCAGCTCGGACCTCTGGACGT 300
QY 308 GTGTTTGGCCTCAAGTTTCTTAAGCTGCTGTTTATTACTGAAGAAAGAAATGTGCAGAT 367
Db 301 GTGTTTGGCCTCAAGTTTCTTAAGCTGCTGTTTATTACTGAAGAAAGAAATGTGCAGAT 360
QY 368 TGTGTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCAGCTATAACAACTTTGGGAA 427
Db 361 TGTGTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCAGCTATAACAACTTTGGGAA 420
QY 428 GAGCATGGACAGCATAGGAAGAAAGAAATATATCAGGTCCAGCATGGTCTCTGAGGTACAC 487
Db 421 GAGCATGGACAGCATAGGAAGAAAGAAATATATCAGGTCCAGCATGGTCTCTGAGGTACAC 480
QY 488 TTTCTCTCTGCCAGAGATGGACAACTGCGCTCTTCTTCCAGCCCTCAGTGTCCAATGC 547
Db 481 TTTCTCTCTGCCAGAGATGGACAACTGCGCTCTTCTTCCAGCCCTCAGTGTCCAATGC 540
QY 548 TGTGCAGAGGGACGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTGCAAGTGTGGA 607
Db 541 TGTGCAGAGGGACGCGCGCTCGAATACGATGACTCGGTGCGAGAGGCTGCAAGTGTGGA 600
QY 608 GAAACATCATGGAACCAACACACTCAGTGGCTAATGAAGCTTGAGAAATTTATATCCAGGACAA 667
Db 601 GAAACATCATGGAACCAACACACTCAGTGGCTAATGAAGCTTGAGAAATTTATATCCAGGACAA 660
QY 668 CATGAAGAAAGAAATGGTAGATACAGCAGAAATGCAGTACAGAACCCAGACGGCTGTGAT 727
Db 661 CATGAAGAAAGAAATGGTAGATACAGCAGAAATGCAGTACAGAACCCAGACGGCTGTGAT 720
QY 728 GATAGAAATAGGACAAACCTGTTGAAACCAACAGCTGAGCAACCGGAAAGTAACTGA 787
Db 721 GATAGAAATAGGACAAACCTGTTGAAACCAACAGCTGAGCAACCGGAAAGTAACTGA 780
QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCACGAGACTTGAACCTTCAGCTCTTGGAAACCTC 847
Db 781 TGTGGAAGCCCAAGTATTAAATCAGACCACGAGACTTGAACCTTCAGCTCTTGGAAACCTC 840
QY 848 CCTCTCGCAACAAATTTGGAAAAACAGATTTTGGACAGACCACTGAAATTAACAAAT 907
Db 841 CCTCTCGCAACAAATTTGGAAAAACAGATTTTGGACAGACCACTGAAATTAACAAAT 900
QY 908 GCAAGATAGACACTGTTCCCTAGAAAGAGGTGTAGCTATGGAAGCAACACATCAT 967

[illegible]

QY 2108 GAATCAGACTGACAGTTTACAGACGCTGTGTCTCAACCAAGAAATGTTATGTCAGATTT 2167
DB 2101 GAATCAGACTGACAGTTTACAGACGCTGTGTCTCAACCAAGAAATGTTATGTCAGATTT 2160
QY 2168 ATCAGTAATAACTGGAACAAACACACTTATGTTATACATACATCATCTTGAACCT 2227
DB 2161 ATCAGTAATAACTGGAACAAACACACTTATGTTATACATACATCATCTTGAACCT 2220
QY 2228 GCATTCTCTGACACTGTTTATACACTGTGTAATACCCATATGTCCT 2276
DB 2221 GCATTCTCTGACACTGTTTATACACTGTGTAATACCCATATGTCCT 2269

RESULT 14

ADSI3801

ID ADS13801 standard; DNA; 2269 BP.

XX AC ADS13801;

XX DT 02-DEC-2004 (first entry)

XX DE Human angiotensin-2 (Ang-2) encoding DNA.

XX KW Ang-1; extracellular matrix; ECM; angiotensin; cytostatic; vasotropic;
XX KW antidiabetic; antiarthritic; cerebroprotective; antiangiogenic;
XX KW gene therapy; human; gene; Ang-2; ds.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT CDS 350..1940

XX FT /*tag= a

XX FT /product= "Ang-2"

XX PN WO2004076650-A2.

XX PD 10-SEP-2004.

XX PF 27-FEB-2004; 2004WO-US006101.

XX PR 27-FEB-2003; 2003US-0450582P.

XX PA (UYPE-) UNIV PENNSYLVANIA.

XX PI Yu Q;

XX PS WPI; 2004-653413/63.

XX DR P-PSDB; ADS13783.

XX PT New pharmaceutical composition comprises a pharmaceutical carrier and an
XX PT amount of an extracellular matrix (ECM)-binding fragment of Ang-1 protein
XX PT or a mutant Ang-1, useful for treating, e.g. cancer, vascular disease, or
XX PT ischemia.

XX PS Disclosure; SEQ ID NO 33; 114pp; English.

XX CC The invention relates to a pharmaceutical composition comprising a
XX CC pharmaceutical carrier and an amount of an extracellular matrix (ECM)-
XX CC binding fragment of angiotensin (Ang)-1 protein or a mutant Ang-1. Also
XX CC provided are methods of treating an individual suspected of having
XX CC coronary artery disease, vascular disease or a condition involving
XX CC ischemia; of promoting angiogenesis, endothelial survival and
XX CC maintaining vascular integrity in an individual; of treating an
XX CC individual suspected of having a disease related to lack of blood vessels
XX CC to effectively promote angiogenesis in the patients with the diseases
XX CC related to lack of blood vessels such as ischemia in hearts and limbs;
XX CC to reduce stroke, heart attack, blood vessel blockage, haemorrhage,
XX CC atherosclerosis risk by maintaining the health and integrity of blood
XX CC vessels; to assist the recovery of the patients who had stroke and the
XX CC angioplasty procedure by promoting the growth/survival of endothelial
XX CC cells and establish endothelial monolayer and inhibit excessive
XX CC inflammation, haemorrhage, and proliferation of vascular smooth muscle;

CC to treat patients with restenosis by inhibiting re-closure of blood
CC vessel after inserting stents into blood vessels; to make stable and
CC functional artificial blood vessels comprising using the composition
CC above; of identifying compounds that modulates binding of Ang-1 to ECM;
CC of treating an individual suspected of having cancer; of preventing
CC diabetes and/or arthritis in an individual suspected of being at risk of
CC developing diabetes or arthritis. The pharmaceutical composition is
CC useful for treating diseases and disorders, e.g. cancer, coronary artery
CC disease, vascular disease, ischaemia, restenosis, diabetes, stroke,
CC angiogenesis, or arthritis. The present sequence represents the human Ang
CC -2 encoding DNA.

XX SQ Sequence 2269 BP; 742 A; 495 C; 518 G; 514 T; 0 U; 0 Other;

Query Match 99.4%; Score 2269; DB 13; Length 2269;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGTATCTCTCCAGCCTTGAGGAGGGAACACACTGTAGGATCTGGGG 67

DB 1 TGGGTTGGTGTATCTCTCCAGCCTTGAGGAGGGAACACACTGTAGGATCTGGGG 60

QY 68 AGAGAGGAACAAGGACCGTGAAGCTCTCTAAAGCTGACAGAGCCCTCCCAAGTG 127

DB 61 AGAGAGGAACAAGGACCGTGAAGCTCTCTAAAGCTGACAGAGCCCTCCCAAGTG 120

QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGGGAGAGAACAG 187

DB 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGCTGGGAGAGAACAG 180

QY 188 CAGTAAACCAGGTTTGTCTGGAAGAGGAAAGAGAGACTTTCATTCAGCGACC 247

DB 181 CAGTAAACCAGGTTTGTCTGGAAGAGGAAAGAGAGACTTTCATTCAGCGACC 240

QY 248 CAGCCATGCGAGGTAGCAGCCCTGCTTTCAGACGCGCAGCTCGGGACTCTGACGT 307

DB 241 CAGCCATGCGAGGTAGCAGCCCTGCTTTCAGACGCGCAGCTCGGGACTCTGACGT 300

QY 308 GTGTTTGCCTCAAGTTTGTCTAGCTGCTGTTTATTACTGAAGAAGAAATGTGGCAGAT 367

DB 301 GTGTTTGCCTCAAGTTTGTCTAGCTGCTGTTTATTACTGAAGAAGAAATGTGGCAGAT 360

QY 368 TGTGTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCCCTATACAACTTTCGGA 427

DB 361 TGTGTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCCCTATACAACTTTCGGA 420

QY 428 GAGCATGGACAGCATAGGAAGCAATATCAGGTCACAGTGGTCTTCGAGCTACAC 487

DB 421 GAGCATGGACAGCATAGGAAGCAATATCAGGTCACAGTGGTCTTCGAGCTACAC 480

QY 488 TTTCTCTCTCCAGAGATGGACAACTGCCGCTCTTCTCCAGCCCTTACGTGTCCAATGC 547

DB 481 TTTCTCTCTCCAGAGATGGACAACTGCCGCTCTTCTCCAGCCCTTACGTGTCCAATGC 540

QY 548 TGTGCGAGGGAGCGCGCGCTCGAATACGATGATCGGTGCGAGAGGCTGCAAGTCTGGA 607

DB 541 TGTGCGAGGGAGCGCGCGCTCGAATACGATGATCGGTGCGAGAGGCTGCAAGTCTGGA 600

QY 608 GAACATCATGGAACAAACACTCAGTGGCTTAATGAAGCTTGAAGATTTATATCCAGGACAA 667

DB 601 GAACATCATGGAACAAACACTCAGTGGCTTAATGAAGCTTGAAGATTTATATCCAGGACAA 660

QY 668 CATGAAGAAGAAATGTTAGAGATACAGCAAGATGCAAGTACAGAACAGACGCGTGTGAT 727

DB 661 CATGAAGAAGAAATGTTAGAGATACAGCAAGATGCAAGTACAGAACAGACGCGTGTGAT 720

QY 728 GATAGAAATAGGACAAACCTGTTGAACCAAACAGCTGAGCAACACGCGGAAGTTAATGA 787

DB 721 GATAGAAATAGGACAAACCTGTTGAACCAAACAGCTGAGCAACACGCGGAAGTTAATGA 780

QY 788 TGTGGAAGCCCAAGTATTAAATCAGACCCAGAGACTTGAAGTTCAGCTCTTGGAACTC 847

DB 781 TGTGGAAGCCCAAGTATTAAATCAGACCCAGAGACTTGAAGTTCAGCTCTTGGAACTC 840

QY	848	CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACACAGACAGTGAATAAACAATTT	907	QY	1928	CTGTGCTCTTTCACCAACAGAGGCGGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA	1987
DB	841	CTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACACAGACAGTGAATAAACAATTT	900	DB	1921	CTGTGCTCTTTCACCAACAGAGGCGGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA	1980
QY	908	GCAAGATAGAACAGTTTCTTAGAAAAAGAGTGCTAGCTATGGAAGACAACATCAT	967	QY	1988	GATTAGAGCCTGTAAACTTTATCACTTAAACTTTGATGATCACTTAAACGGACCAAGCAAGAC	2047
DB	901	GCAAGATAGAACAGTTTCTTAGAAAAAGAGTGCTAGCTATGGAAGACAACATCAT	960	DB	1981	GATTAGAGCCTGTAAACTTTATCACTTAAACTTTGATGATCACTTAAACGGACCAAGCAAGAC	2040
QY	968	CCAACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAACGACAAA	1027	QY	2048	CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA	2107
DB	961	CCAACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAACGACAAA	1020	DB	2041	CCTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA	2100
QY	1028	TTCCATCATTTAGAACTAGAAAAAATAAGTGTGCTGACCGGTGAATAATTCAGTTCT	1087	QY	2108	GAATCAGACTGACAGTTTACAGAGCGTGTGTCACCAACCAAGAAATTTATGTCGAAGTTT	2167
DB	1021	TTCCATCATTTAGAACTAGAAAAAATAAGTGTGCTGACCGGTGAATAATTCAGTTCT	1080	DB	2101	GAATCAGACTGACAGTTTACAGAGCGTGTGTCACCAACCAAGAAATTTATGTCGAAGTTT	2160
QY	1088	TCAAAAGCAGCAACATGATCTCATGGAGACATTAATAACTTACTGATGATGTCAC	1147	QY	2168	ATCAGTAAATAACTCGAAAAACAGAACACTTATGTTATATACATACAGATCATCTTGAAC	2227
DB	1081	TCAAAAGCAGCAACATGATCTCATGGAGACATTAATAACTTACTGATGATGTCAC	1140	DB	2161	ATCAGTAAATAACTCGAAAAACAGAACACTTATGTTATATACATACAGATCATCTTGAAC	2220
QY	1148	ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAGAACAAATCAGCTTCAGAGACTG	1207	QY	2228	GCATTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCTCT	2276
DB	1141	ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAGAGAACAAATCAGCTTCAGAGACTG	1200	DB	2221	GCATTCTTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCTCT	2269
QY	1208	TGCTGAAGTATTTCAAAATCAGGACACACCAAAATGGCATCTACAGCTTAAACATTCCTTAA	1267	RESULT 15			
DB	1201	TGCTGAAGTATTTCAAAATCAGGACACACCAAAATGGCATCTACAGCTTAAACATTCCTTAA	1260	ID	ABX63023		
QY	1268	TTCTACAGAAAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGCGGTGGACAAAT	1327	XX	ABX63023 standard; cDNA; 2384 BP.		
DB	1261	TTCTACAGAAAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGCGGTGGACAAAT	1320	AC	ABX63023;		
QY	1328	TATTTCAGGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGT	1387	DT	25-FEB-2003 (first entry)		
DB	1321	TATTTCAGGACGTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGATATAAAGT	1380	XX	Human cDNA #23 differentially expressed in activated vascular tissue.		
QY	1388	GGGATTTGGTAACCCCTTCAGGAGAAATATTGGCTGGGAATAGTTTGTTCGCAACTGCAC	1447	XX	Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;		
DB	1381	GGGATTTGGTAACCCCTTCAGGAGAAATATTGGCTGGGAATAGTTTGTTCGCAACTGCAC	1440	KW	hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;		
QY	1448	TAACTCAGCAACCTATGTGCTTAAATAACACCTTAAAGCTGGGAAGGAATGAGGCTTA	1507	KW	gene therapy; vascular disease; cancer; coronary; artery disease;		
DB	1441	TAACTCAGCAACCTATGTGCTTAAATAACACCTTAAAGCTGGGAAGGAATGAGGCTTA	1500	KW	hypertension; diabetes; pre-eclampsia; restenosis;		
QY	1508	CTCATTTGATGAACATTTCTATCTCTCAAGTGAAGACTCAATTTATAGATTCACCTTAA	1567	XX	ischaemia-reperfusion injury; stroke.		
DB	1501	CTCATTTGATGAACATTTCTATCTCTCAAGTGAAGACTCAATTTATAGATTCACCTTAA	1560	OS	Homo sapiens.		
QY	1568	AGGACTTACAGGACAGCGCGCAAAATAAGCAGCATCAGCCAACAGGAAATGATTTTAG	1627	XX			
DB	1561	AGGACTTACAGGACAGCGCGCAAAATAAGCAGCATCAGCCAACAGGAAATGATTTTAG	1620	PN	US2002137081-A1.		
QY	1628	CACAAAGGATGAGACAACGACAAATGATTTGCAAAATGTTTCAAAATGCTTAACAGGAGG	1687	PD	26-SEP-2002.		
DB	1621	CACAAAGGATGAGACAACGACAAATGATTTGCAAAATGTTTCAAAATGCTTAACAGGAGG	1680	XX	08-JAN-2002; 2002US-00044090.		
QY	1688	CTGGTGGTTTGTATGATGTGGTCTTCCAACTTGAACCGAATGTACTATCCACAGAGCA	1747	XX	28-JUL-2000; 2000US-0222469P.		
DB	1681	CTGGTGGTTTGTATGATGTGGTCTTCCAACTTGAACCGAATGTACTATCCACAGAGCA	1740	PR	08-JAN-2001; 2001US-0260483P.		
QY	1748	GAAACAAATAAGTTTCAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCTATTGCT	1807	XX	(BAND/) BANDMAN O.		
DB	1741	GAAACAAATAAGTTTCAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCTATTGCT	1800	XX	Bandman O;		
QY	1808	CAAGGCGCAACCATGATGATCCGACAGCAATTTCTAAACATCCAGTCCACCTGAGG	1867	XX	WPI; 2003-110597/10.		
DB	1801	CAAGGCGCAACCATGATGATCCGACAGCAATTTCTAAACATCCAGTCCACCTGAGG	1860	PT	Combination for diagnosing, staging, treating, or monitoring the		
QY	1868	AACTCTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACCTGGAAGTCAACGGCTGGCA	1927	PT	progression of treatment of a vascular disease, e.g. atherosclerosis,		
DB	1861	AACTCTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCACCTGGAAGTCAACGGCTGGCA	1920	PT	comprises several cDNAs that are differentially expressed in activated		
				PT	vascular tissue.		
				XX	Claim 1; Page; 18pp; English.		
				XX	This invention relates to a combination comprising several cDNAs that are		
				CC	differentially expressed in activated vascular tissue. The invention also		
				CC	discloses a high throughput method for detecting differentially expressed		
				CC	cDNAs in a sample. The cDNAs of the invention may have		
				CC	antiatheriosclerotic; cytostatic; cardiant; hypotensive; antidiabetic;		
				CC	gynaecological; vasotropic and cerebroprotective activities and may be		
				CC	used in gene therapy. The cDNAs of the invention may be used in a high-		
				CC	throughput methods for detecting differential expression of one or more		

CC cDNAs in a sample, or screening several molecules or compounds to
CC identify a molecule or compound that specifically binds a cDNA of the
CC invention. A protein encoded by the cDNA may be used to screen several
CC molecules or compounds to identify a ligand that specifically binds to
CC the protein, or to produce or purify an antibody to the protein that can
CC be used to detect a protein in a sample or purify a natural or
CC recombinant protein from a sample. The nucleotides may be useful for
CC diagnosing, staging, treating, or monitoring the progression of treatment
CC of a vascular disease, e.g. atherosclerosis, cancer, coronary artery
CC disease, hypertension, diabetes, pre-eclampsia, ischaemia-reperfusion
CC injury, restenosis, or stroke. The cDNAs can also be used for large-scale
CC genetic or gene expression analysis of several new nucleic acid
CC molecules. Antibodies to the proteins encoded by the cDNAs are useful for
CC diagnosing pre-pathologic disorders, and chronic or acute diseases
CC associated with abnormalities in the expression, amount or distribution
CC of the protein. The present sequence represents a cDNA of the invention
CC that is differentially expressed in activated vascular tissue. Note: The
CC sequence data for this patent did not form part of the specification, but
CC was obtained in electronic format directly from USPTO at
CC <http://seqdata.uspto.gov/sequence.html?docID=20020137081>
XX
SQ Sequence 2384 BP; 797 A; 508 C; 533 G; 546 T; 0 U; 0 Other;

Query Match 97.9%; Score 2233.6; DB 8; Length 2384;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 2239; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY	35	TTGAGGGGGAACACACGTGTAGGATCTGGGAGAGAGAGAACAAAGGACCGTGAAGCT	94
DB	9	TTGATTCGGATATGACACTGTAGGATCTGGGAGAGAGAGAACAAAGGACCGTGAAGCT	69
QY	95	GCTCTGTAAAGCTGACACAGCCCTCCCAAGTGAAGGAGGACTGTTCTTCCACTGCAATC	154
DB	69	GCTCTGTAAAGCTGACACAGCCCTCCCAAGTGAAGGAGGACTGTTCTTCCACTGCAATC	128
QY	155	TGACAGTTTACTGATCGCTCGGAGAGAAACACAGAGTAAACACAGGTTGCTACTGGAA	214
DB	129	TGACAGTTTACTGATCGCTCGGAGAGAAACACAGAGTAAACACAGGTTGCTACTGGAA	188
QY	215	AAAGAGGAAGAGAGACTTTCATTCAGCGGACCCAGCCATGGCAGCGTAGCAGCCCTGCG	274
DB	189	AAAGAGGAAGAGAGACTTTCATTCAGCGGACCCAGCCATGGCAGCGTAGCAGCCCTGCG	248
QY	275	TTTCAGACGGCAGCAGCTCGGAGACTCTGGAAGTGTGTTTCCCTCAAGTTTGTCTAAGCTG	334
DB	249	TTTCAGACGGCAGCAGCTCGGAGACTCTGGAAGTGTGTTTCCCTCAAGTTTGTCTAAGCTG	308
QY	335	CTGGTTTATTAATGAAGAAAGATGTGGAGATTTGTTTCTTCTGAGCTGTGATCT	394
DB	309	CTGGTTTATTAATGAAGAAAGATGTGGAGATTTGTTTCTTCTGAGCTGTGATCT	368
QY	395	TGTTCTGGCCGAGCCCTATTAACACTTTCGGAAGGAGCATGAGCAGCATAGGAAGAGCA	454
DB	369	TGTTCTGGCCGAGCCCTATTAACACTTTCGGAAGGAGCATGAGCAGCATAGGAAGAGCA	428
QY	455	ATATCAGGTCAGCATGGGTCCTGACGTACACTTTCCTCTGCGAGAGATGGACAACTG	514
DB	429	ATATCAGGTCAGCATGGGTCCTGACGTACACTTTCCTCTGCGAGAGATGGACAACTG	488
QY	515	CCGCTCTTCTCCAGCCCTTACGTTTCCATGTGTGCGAGGAGCCGCGCGCTCGAATA	574
DB	489	CCGCTCTTCTCCAGCCCTTACGTTTCCATGTGTGCGAGGAGCCGCGCGCTCGAATA	548
QY	575	CGATGATCCGTCAGAGGCTGCAAGTCTGGAGACATCATGGAACCACTCAGTG	634
DB	549	CGATGATCCGTCAGAGGCTGCAAGTCTGGAGACATCATGGAACCACTCAGTG	608
QY	635	GCTAATCAAGCTTGAGAAATATATCCAGAGCAACATGAAGAAAGAAATGGTAGAGATACA	694
DB	609	GCTAATCAAGCTTGAGAAATATATCCAGAGCAACATGAAGAAAGAAATGGTAGAGATACA	668
QY	695	GCAGAAATGCAGTACAGAACCGAGCGGTGTGATGATAGAAATAGGGAACAACTGTTGAA	754

DB	669	GCAGAAATGCAGTACAGAACCGAGCGGTGTGATGATAGAAATAGGGAACAACTGTTGAA	728
QY	755	CCAAACAGCTGAGCAAAACCGGAAGTTAACTGATGTGGAAGCCCAAGTATTAATCAGAC	814
DB	729	CCAAACAGCTGAGCAAAACCGGAAGTTAACTGATGTGGAAGCCCAAGTATTAATCAGAC	788
QY	815	CACGAGCTTGAACCTTCAGCTCTTGGAAACACTCCCTCTCGAACAACAAATTTGAAAAACA	874
DB	789	CACGAGCTTGAACCTTCAGCTCTTGGAAACACTCCCTCTCGAACAACAAATTTGAAAAACA	848
QY	875	GATTTTGGACACAGACCCAGTGAATAAACAATTTGCAAGATTAAGAACAGATTTCTAGAAA	934
DB	849	GATTTTGGACACAGACCCAGTGAATAAACAATTTGCAAGATTAAGAACAGATTTCTAGAAA	908
QY	935	GAAGTGCTAGCTATGGAAGACAAGACATATCCAACTACAGTCAATTAAGAACAGAA	994
DB	909	GAAGTGCTAGCTATGGAAGACAAGACATATCCAACTACAGTCAATTAAGAACAGAA	968
QY	995	AGATCAGCTACAGGTTAGTATCCAAAGCAAAATTCATCATTTGAAGAACTAGAAAAAA	1054
DB	969	AGATCAGCTACAGGTTAGTATCCAAAGCAAAATTCATCATTTGAAGAACTAGAAAAAA	1028
QY	1055	AATAGTGACTGCCACCGTGAATAAATTCAGTTCTTCAAAAAGCAGCAACATGATCTCATGA	1114
DB	1029	AATAGTGACTGCCACCGTGAATAAATTCAGTTCTTCAAAAAGCAGCAACATGATCTCATGA	1088
QY	1115	GACAGTTAATACTTACTGACTATGATGCCACATCAAACTCAGCTAAGGACCCCACTGT	1174
DB	1089	GACAGTTAATACTTACTGACTATGATGCCACATCAAACTCAGCTAAGGACCCCACTGT	1148
QY	1175	TGCTAAAGAAAGACAATCAGCTTCAGAGACTGTGCTGAAGTATTAATCAAACTCAGGACAC	1234
DB	1149	TGCTAAAGAAAGACAATCAGCTTCAGAGACTGTGCTGAAGTATTAATCAAACTCAGGACAC	1208
QY	1235	CACAAATGSCATCTACACGTTTAACTTCCCTAACTTACAGAAAGAGATCAAGGCTACTG	1294
DB	1209	CACAAATGSCATCTACACGTTTAACTTCCCTAACTTACAGAAAGAGATCAAGGCTACTG	1268
QY	1295	TGACATGGAAGCTGGAGGCGGGTGGACAAATTTACAGCGACGTGAGGATGGCAGCGT	1354
DB	1269	TGACATGGAAGCTGGAGGCGGGTGGACAAATTTACAGCGACGTGAGGATGGCAGCGT	1328
QY	1355	TGATTTTTCAGAGACTTGGAAAGAAATATAAGTGGGATTTGGTAAACCTTTCAGGAGATA	1414
DB	1329	TGATTTTTCAGAGACTTGGAAAGAAATATAAGTGGGATTTGGTAAACCTTTCAGGAGATA	1388
QY	1415	TTGGCTGGGAAATAGTGTTCGCAACTGACTAATCAGCAACGCTATGCTGTAAAT	1474
DB	1389	TTGGCTGGGAAATAGTGTTCGCAACTGACTAATCAGCAACGCTATGCTGTAAAT	1448
QY	1475	ACACCTTAAAGACTGGGAAAGGAAATGAGGCTTACTCATTTGATGAACATTTCTATCTC	1534
DB	1449	ACACCTTAAAGACTGGGAAAGGAAATGAGGCTTACTCATTTGATGAACATTTCTATCTC	1508
QY	1535	AAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTACAGGAGACGCGGCAAAAT	1594
DB	1509	AAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTACAGGAGACGCGGCAAAAT	1568
QY	1595	AAGCAGCATCAGCAACACAGGAAATGATTTTAGCACAAGAGATGGAGACAACCAAAATG	1654
DB	1569	AAGCAGCATCAGCAACACAGGAAATGATTTTAGCACAAGAGATGGAGACAACCAAAATG	1628
QY	1655	TATTTGCAAAATGTTCAAAATGCTAAACAGGAGCTGGTGGTGTGATGATGCTCTTC	1714
DB	1629	TATTTGCAAAATGTTCAAAATGCTAAACAGGAGCTGGTGGTGTGATGATGCTCTTC	1688
QY	1715	CAACTTGAACCGGAATGTACTATCCACAGGAGGAGACACAATAAGTTTCAACGCGATTAA	1774
DB	1689	CAACTTGAACCGGAATGTACTATCCACAGGAGGAGACACAATAAGTTTCAACGCGATTAA	1748
QY	1775	ATGGTACTACTGGAAGGCTCAGGCTATTCGCTCAAGGCGCACCAACCATGATGATCCGACC	1834
DB	1749	ATGGTACTACTGGAAGGCTCAGGCTATTCGCTCAAGGCGCACCAACCATGATGATCCGACC	1808

QY	1835	AGCAGATTTCTAAACATCCAGTCCACCTGAGGAACTGTCTCGAACTATTTTCAAAGACT	1894
Db	1809	AGCAGATTTCTAAACATCCAGTCCACCTGAGGAACTGTCTCGAACTATTTTCAAAGACT	1868
QY	1895	TAAGCCAGTGCACATGAAAGTCAAGGCTGCGGACCTGTGTCTCTCCACCACAGAGGGCG	1954
Db	1869	TAAGCCAGTGCACATGAAAGTCAAGGCTGCGGACCTGTGTCTCTCCACCACAGAGGGCG	1928
QY	1955	TGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATTAGAGCTGTAAACTTTTATCACTT	2014
Db	1929	TGTGCTCGGTGCTGACGGGACCCACATGCTCCAGATTAGAGCTGTAAACTTTTATCACTT	1988
QY	2015	AAACTTGCATCACTTAAACGACCAAGCAAGACCCCTAAACATCCATAATTGTGATTAGAC	2074
Db	1989	AAACTTGCATCACTTAAACGACCAAGCAAGACCCCTAAACATCCATAATTGTGATTAGAC	2048
QY	2075	AGAACACCTATGCAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCT	2134
Db	2049	AGAACACCTATGCAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGACGCT	2108
QY	2135	GCTGTCAACAACCAAGATGTTATGTGCAAGTTTATCAGTAAATAACTGGAAAACAGAAACA	2194
Db	2109	GCTGTCAACAACCAAGATGTTATGTGCAAGTTTATCAGTAAATAACTGGAAAACAGAAACA	2168
QY	2195	CTTATGTTATACAATACAGATCATCTTGGAACTGCAATTTCTTGAGCACTGTTTATACAC	2254
Db	2169	CTTATGTTATACAATACAGATCATCTTGGAACTGCAATTTCTTGAGCACTGTTTATACAC	2228
QY	2255	TGTGTAATACCCATATGTCCTGAATTC	2282
Db	2229	TGTGTAATACCCATATGTCCTGAATTC	2256

Search completed: July 29, 2005, 03:19:05
Job time : 1311.44 secs

QY	125	GTGAGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTCGAGGAGAA	184
Db	61	GTGAGCAGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTCGAGGAGAA	120
QY	185	CAGCAGTAAACACAGGTTTGTCTACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	244
Db	121	CAGCAGTAAACACAGGTTTGTCTACTGGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG	180
QY	245	ACCCAGCCATGCGAGCGTAGCAGCCCTGCTGTTTTCAGAGCGCAGCAGCTCGGAGCTCTGGA	304
Db	181	ACCCAGCCATGCGAGCGTAGCAGCCCTGCTGTTTTCAGAGCGCAGCAGCTCGGAGCTCTGGA	240
QY	305	CGTGTGTTTCCCTCAAGTTTCTAAGCTGCTGGTTTATTTACTGAGAGAGAGAGAGAGAG	364
Db	241	CGTGTGTTTCCCTCAAGTTTCTAAGCTGCTGGTTTATTTACTGAGAGAGAGAGAGAGAG	300
QY	365	GATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCGCTATAACAACTTTTCG	424
Db	301	GATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGGAGCGCTATAACAACTTTTCG	360
QY	425	GAAGAGATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCTGAGCTTA	484
Db	361	GAAGAGATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCTGAGCTTA	420
QY	485	CACCTTCTCTCCAGAGATGGACAACTGCCGCTCTTCTCCAGCCCTACGTTGCCAA	544
Db	421	CACCTTCTCTCCAGAGATGGACAACTGCCGCTCTTCTCCAGCCCTACGTTGCCAA	480
QY	545	TGCTGTGAGAGGAGCGCGCTGGAATACAGATGATCGGTGCGAGAGCTGCAAGTGTCT	604
Db	481	TGCTGTGAGAGGAGCGCGCTGGAATACAGATGATCGGTGCGAGAGCTGCAAGTGTCT	540
QY	605	GGAGAACATCATGGGAAAACAACTCAGTGGCTTAATGAAGCTTTGAGAAATATATCCAGGA	664
Db	541	GGAGAACATCATGGGAAAACAACTCAGTGGCTTAATGAAGCTTTGAGAAATATATCCAGGA	600
QY	665	CAACATGAAGAGAGAAATGGTAGATACAGAGAGATGCAGTACAGAACCCAGACGGCTGT	724
Db	601	CAACATGAAGAGAGAAATGGTAGATACAGAGAGATGCAGTACAGAACCCAGACGGCTGT	660
QY	725	GATGATAGAAATAGGAGCAAACTGTTGAAACAAACAGCTGAGCAAAACCGGAAAGTTAAC	784
Db	661	GATGATAGAAATAGGAGCAAACTGTTGAAACAAACAGCTGAGCAAAACCGGAAAGTTAAC	720
QY	785	TCAGTGGAGCCCAAGTATTAAATCAGACACGAGACTTTGAACCTTCAGCTCTTGGAA	844
Db	721	TCAGTGGAGCCCAAGTATTAAATCAGACACGAGACTTTGAACCTTCAGCTCTTGGAA	780
QY	845	CTCCCTCTCGCAAAACAAATTTGAAAAACAGATTTTGGACCAAGACCCAGTGAATTAACAA	904
Db	781	CTCCCTCTCGCAAAACAAATTTGAAAAACAGATTTTGGACCAAGACCCAGTGAATTAACAA	840
QY	905	ATTGCAAGATAGACAGTTTCTAGAAAGAGGTGTAGCTATGGAAGAGCAAGCAAT	964
Db	841	ATTGCAAGATAGACAGTTTCTAGAAAGAGGTGTAGCTATGGAAGAGCAAGCAAT	900
QY	965	CATCCAACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAAGCA	1024
Db	901	CATCCAACTACAGTCAATAAAGAGAGAGAGATCAGCTACAGGTGTAGTATCAAGCA	960
QY	1025	AAATTCATCATTTGAAGAACTAGAAAAAATAAGTACTGCGCCAGCGTGAATTAATTCAGT	1084
Db	961	AAATTCATCATTTGAAGAACTAGAAAAAATAAGTACTGCGCCAGCGTGAATTAATTCAGT	1020
QY	1085	TCTTCAAGAGAGCAACATGATCTCATGAGAGAGAGATTAATTAATTAATTAATTAATTAAT	1144
Db	1021	TCTTCAAGAGAGCAACATGATCTCATGAGAGAGAGATTAATTAATTAATTAATTAATTAAT	1080
QY	1145	CACATCAAACTCAGCTTAAGGACCCCACTGTTCTTAAAGAGAGAGAGAGAGAGAGAGAG	1204
Db	1081	CACATCAAACTCAGCTTAAGGACCCCACTGTTCTTAAAGAGAGAGAGAGAGAGAGAGAG	1137

RESULT 2

BC022490

LOCUS

DEFINITION Homo sapiens cDNA clone IMAGE:4792831, containing frame-shift

2083 bp mRNA linear

HTC 12-OCT-2004

errors.	
ACCESSION	BC022490
VERSION	BC022490.1
KEYWORDS	GI:18490680
SOURCE	HTC
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	1 (bases 1 to 2083) Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G., Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zeeberg, B., Buettow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Sapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Usdin, T.B., Toohiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.
TITLE	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED	12477932
REFERENCE	2 (bases 1 to 2083) Director MGC Project.
AUTHORS	Direct Submission
TITLE	Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL) DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: http://www-shgc.stanford.edu Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.
FEATURES	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LILNL at: http://image.llnl.gov Series: IRAP Plate: 32 Row: b Column: 11 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557314 This clone has the following problem: frame shifted. Location/Qualifiers 1..2083 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:472831" /tissue_type="Brain, hypothalamus" /clone_lib="NIH_MGC_96" /lab_host="DH10B" /note="Vector: pBluescript"
source	
ORIGIN	
Query Match	88.9%; Score 2029.2; DB 3; Length 2083;
Best Local Similarity	99.4%; Pred. No. 0;
Matches 2058; Conservative	0; Mismatches 8; Indels 4; Gaps 2;
162	TTACTGATGCTCTGGAGAGAAACACAGCAGTAAACACAGGTTTGCTACTGCGAAAGAGG 221
3	TTACTGATGCTCTGGAGAGAAACACAGCAGTAAACACAGGTTTGCTACTGCGAAAGAGG 62
222	AAAGAGAAGACTTTTCAATTCAGCGACCCAGCCATGGCAGCGTAGCAGCCCTCGCTTCAGA 281
63	AAAGAGAAGACTTTTCAATTCAGCGACCCAGCCATGGCAGCGTAGCAGCCCTCGCTTCAGA 122
282	CGGCAGCAGCTCGGGACTCTCGGACGTGTGTGTCCTCAAGTTTGTGAAGCTGCTGCTTT 341
123	CGGCAGCAGCTCGGGACTCTCGGACGTGTGTGTCCTCAAGTTTGTGAAGCTGCTGCTTT 182
342	ATTACTGAAGAAAGATGTGGCAGATGTTTCTTTTACTCTGAGCTGTGTGATCTTGCTTG 401
183	ATTACTGAAGAAAGATGTGGCAGATGTTTCTTTTACTCTGAGCTGTGTGATCTTGCTTG 242
402	GCCGACGCTTATTAACACTTTTCGAGAGAGCATGAGCAGCATAGGAAGAGCAATATATCAG 461
243	GCCGACGCTTATTAACACTTTTCGAGAGAGCATGAGCAGCATAGGAAGAGCAATATATCAG 302
462	GTCCAGCATGGGTCTCTGACGTACACTTCTCTGCGCAGAGATGGACAACTGCGCTCT 521
303	GTCCAGCATGGGTCTCTGACGTACACTTCTCTGCGCAGAGATGGACAACTGCGCTCT 362
522	TCCTCCAGCCCTTACGTGTCCAATGCTGTGAGAGGACCGCGCTCGAATACGATGAC 581
363	TCCTCCAGCCCTTACGTGTCCAATGCTGTGAGAGGACCGCGCTCGAATACGATGAC 422
582	TCGGTCGAGGCTGCAAGTCTGGAGAACATCATGGAAACAACTCATGCTAGTGCTTAATG 641
423	TCGGTCGAGGCTGCAAGTCTGGAGAACATCATGGAAACAACTCATGCTAGTGCTTAATG 482
642	AAGCTTGAGATTTATATCCAGGACCAACATCAAGAAAGAAATGGTAGAGATACAGCAAT 701
483	AAGCTTGAGATTTATATCCAGGACCAACATCAAGAAAGAAATGGTAGAGATACAGCAAT 542
702	GCAGTACAGAACCCAGACGGCTGTGATGATAGAAATAGGGACAAACCTGTTGAACCAACA 761
543	GCAGTACAGAACCCAGACGGCTGTGATGATAGAAATAGGGACAAACCTGTTGAACCAACA 602
762	GCTGAGCAACCGGGAAGTTAACTGATGTGGAGCCCAAGTATTAATACAGACACAGCA 821
603	GCTGAGCAACCGGGAAGTTAACTGATGTGGAGCCCAAGTATTAATACAGACACAGCA 662
822	CTTGAACCTCAGCTCTTTGGAACTCTCCCTCTCGACAAACAAATTTGGAACAAACAGATTTG 881
663	CTTGAACCTCAGCTCTTTGGAACTCTCCCTCTCGACAAACAAATTTGGAACAAACAGATTTG 722
882	GACCAGACCAAGTGAATAAACAATTTGCAAGATAAGAACAGTTTCTCTAGAAAGAGAGTG 941
723	GACCAGACCAAGTGAATAAACAATTTGCAAGATAAGAACAGTTTCTCTAGAAAGAGAGTG 782
942	CTAGCTATGAAGACCAAGCATCATCACTACAGTCAATTAAGAGAGAGAAAGATCAG 1001
783	CTAGCTATGAAGACCAAGCATCATCACTACAGTCAATTAAGAGAGAGAAAGATCAG 842
1002	CTACAGGTGTAGTATCCAAAGCAAAATTTCCATCATTTGAAGAACTAGAAAAAATAAGTG 1061
843	CTACAGGTGTAGTATCCAAAGCAAAATTTCCATCATTTGAGAACTAGAAAAAATAAGTG 902
1062	ACTGCCACCGGTGAATAATTCAGTTTCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTT 1121
903	ACTGCCACCGGTGAATAATTCAGTTTCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTT 962
1122	AATAACTTACTGATATGATGTCCACATCAACTCAGCTAAGGACCCCTGTTGCTTAAA 1181
963	AATAACTTACTGATATGATGTCCACATCAACTCT--CTAAGGACCCCTGTTGCTTAAA 1019
1182	GAAGAACAAATCAGCTTTCAGAGACTGTGCTGAAGTATTTCAATCAGGACACACCAAAAT 1241
1020	GAAGAACAAATCAGCTTTCAGAGACTGTGCTGAAGTATTTCAATCAGGACACACCAAGAT 1079

1242 GGCATCTACAGTGAATTAATCCCTAATCTCAGAGAGATCAAGCCCTACTGTGACATG 1301
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1080 GGCATCTACAGCTTAACATTTCCCTAATCTCAGAGAGATCAAGCCCTACTGTGACATG 1139
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1302 GAAGCTGAGGAGCGGGTGGACAATATTATCAGCAGCTGAGGATGGCAGCGTTGATTTT 1361
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1140 GAAGCTGAGGAGCGGGTGGACAATATTATTCAGCAGCTGAGGATGGCAGCGTTGATTTT 1199
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1362 CAGAGGACTTGGAAAGAAATATAAGTGGGATTTGGTAACCCCTTCAGGAGAAATATTGGCTG 1421
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1200 CAGAGGACTTGGAAAGAAATATAAGTGGGATTTGGTAACCCCTTCAGGAGAAATATTGGCTG 1259
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1422 GGAATAGAGTTTGTTCGCACTGACTAATCAGCAACGCTATGTGCTTAAAAATACACCTT 1481
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1260 GGAATAGAGTTTGTTCGCACTGACTAATCAGCAACGCTATGTGCTTAAAAATACACCTT 1319
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1482 AAAGACTGGGAAGGAATGAGCGTTACTCATTTGTATGAACATTTCTATCTCAAGTGAA 1541
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1320 AAAGACTGGGAAGGAATGAGCGTTACTCATTTGTATGAACATTTCTATCTCAAGTGAA 1379
|||||
1542 GAACTCAATTATAGATTCCACCTTAAAGGACTTACAGGGACAGCGGCAAAAATAAGCAGC 1601
|||||
1380 GAACTCAATTATAGATTCCACCTTAAAGGACTTACAGGGACAGCGGCAAAAATAAGCAGC 1439
|||||
1602 ATCAGCCCAACGAGGAATGATTTTAGCAAAAGGATGGAGACAACGACAAATGTATTTCG 1661
|||||
1440 ATCAGCCCAACGAGGAATGATTTTAGCAAAAGGATGGAGACAACGACAAATGTATTTCG 1499
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1662 AAATGTTCAAAATGCTAACAGAGCGTGGTGGTTGATGCATGTGGTCTTCCAACTTG 1721
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1500 AAATGTTCAAAATGCTAACAGAGCGTGGTGGTTGATGCATGTGGTCTTCCAACTTG 1559
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1722 AACGGAATGCTATCTCCACAGAG-CGAGAAACAATAAGTTTCAACGGCATTAATGGTA 1780
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1560 AACGGAATGCTATCTCCACAGAGAGCAACAAATAAGTTTCAACGGCATTAATGGTA 1619
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1781 CTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCAACCATGATCCGACCAAGCAG 1840
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1620 CTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCAACCATGATCCGACCAAGCAG 1679
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1841 TTTCTTAACATCCGAGTCCACCTGAGGAATCTGTCGAACATATTTTCAAGACTTAAGCC 1900
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1680 TTTCTTAACATCCGAGTCCACCTGAGGAATCTGTCGAACATATTTTCAAGACTTAAGCC 1739
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1901 CAGTGCACCTGAAAGTCACGGCTCGGCACCTGCTCTCTCCACCACAGAGGCGGTGCT 1960
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1740 CAGTGCACCTGAAAGTCACGGCTCGGCACCTGCTCTCTCCACCACATAGGCGGTGCT 1799
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1961 CGGTGCTGACGGGACCCACATGCTCCAGATTAGAGCTGTAAACTTTATCACTTAAACTT 2020
|||||
1800 CGGTGCTGACGGGACCCACATGCTCCAGATTAGAGCTGTAAACTTTATCACTTAAACTT 1859
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2021 GCATCACTTTAAGGACCAAGCAAGCCCTTAACATCCATATTTGATTAGACAGAC 2080
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1860 GCATCACTTTAAGGACCAAGCAAGCCCTTAACATCCATATTTGATTAGACAGAC 1919
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2081 CTTATGCAAGATGAACCCGAGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTC 2140
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1920 CTTATGCAAGATGAACCCGAGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTC 1979
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2141 ACAACCAAGAAATTTATGTGCAAGTTTATCAGTAATAAATCTGAAACAGACACTTATG 2200
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2201 TTATACAAATACAGATCATCTTGGAACTGCA 2230
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2040 TTATACAAATACAGATCATCTTGGAACTGCA 2069
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RESULT 3
AK048622 2443 bp mRNA linear HTC 03-APR-2004
LOCUS
DEFINITION Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched

library, clone:CI30089A05 product:ANGIOPOIETIN-2 PRECURSOR, full insert sequence.
AK048622
AK048622.1 GI:26339449
HTC; CAP trapper.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
99279253
10349636
2
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
Genome Res. 10 (10), 1617-1630 (2000)
20499374
11042159
3
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, K., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Wakahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
Genome Res. 10 (11), 1757-1771 (2000)
20530913
11076861
4
The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection
Nature 409, 685-690 (2001)
5
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2443)
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, P., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)
COMMENT
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

QY	1913	AGTCACGGCTGCGCACTGTGCTCTTCCACACACAGAGGGCGGTGCTCGGTGCTGACGG	1972
Db	1826	AGACAC--CAATGATAGACGCCCTTTCCATCATCAGGAGTGTCTCTCGGGGGTGGGGAG	1883
QY	1973	GACCCACATGCTCCAGATTAGAGCCTGTAAACTTTTATCATCTTAAACTTCATCACTTAAC	2032
Db	1884	GGTCTGTGTGTACCACTGAAGC-----GCATCACTTAAAGCTGCACGGCTTAACC	1934
QY	2033	GGACCAACAGACACCTAAACATCCATTAATTTGTGATTTAGACAGACACCTATGCAAGA	2092
Db	1935	AACCAAGGCACTGCACTCTGGAGAACACTTCTTGGGAG-----	1974
QY	2093	TGAACCCGAGGCTGAGAACTCAGACTGACAGTTTACAGACGCTGTGTCAACACCAAGAA	2152
Db	1975	-----GTTGTGCTGAGATCAGAGACAGCAGCTGCAGAC---TCTGTACAGGGAGAA	2027
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QY	2213	GATCATCTGGAACTGCATTCTCTGAGCACTGTTTATACACTGTGTAATATACCATATG	2272
Db	2088	----ATCTTGGGACCACTTCTCTAAGCACCGTTTCTAGAGTGAATACATTCACAGCTC	2143
QY	2273	TCCTG 2277	
Db	2144	GGCTG 2148	
RESULT 5			
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LOCUS	AY407058	1215 bp	DNA linear
DEFINITION	Homo sapiens ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.		
ACCESSION	AY407058		
VERSION	AY407058.1	GI:39763029	
KEYWORDS	GSS.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 1215) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios		
JOURNAL	Science	302 (5652), 1960-1963 (2003)	
PUBMED	14671302		
REFERENCE	2 (bases 1 to 1215) Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civeello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.		
AUTHORS	Direct Submission		
TITLE	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA		
JOURNAL	This sequence was made by sequencing genomic exons and ordering them based on alignment.		
COMMENT	Location/Qualifiers		
FEATURES	source		
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gene	/gene="ANGPT2"		
	/locus_tag="HCM2764"		
ORIGIN			
Query Match	40.9%;	Score 933.4;	DB 9; Length 1215;
Best Local Similarity	97.3%;	Pred. No. 3.5e-246;	

		/mol_type="mRNA" /db_xref="taxon:9606" /clone="CS01037YG20" /tissue_type="PLACENTA COT 25-NORMALIZED" /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED" /note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN			
Query Match		40.3%; Score 918.8; DB 1; Length 1028;	
Best Local Similarity		96.6%; Pred. No. 3.6e-242;	
Matches		980; Conservative 9; Mismatches 18; Indels 7; Gaps 5;	
QY	1190	AATCAGCTTCAGAGCTGCTGCTGAGTATTCAATCAGGACACACACAAATGGCATCTA	1249
DB	1009	AAATCRSTTCAGARACTGGYTRAA--TWTCAAAATCRGACMCACACGAAT--GCATCTA	953
QY	1250	CACGTTAAACATTCCTTAATCTTACAGAAGAGATCAAGGCTACTGTGACATGGAAGCTGG	1309
DB	952	CAGC-TWACATTCCTTAATCTTACAGAAGAGATCAAGCCCTACTGTAAATGGAAGCTGG	894
QY	1310	AGAGCGGCTGGACAAATTAATTCAGGAGCTGAGAGATGCGAGCTTGAATTTTCAGAGGAC	1369
DB	893	AGGAGCGGCTGGACAAATTAATTCAGGAGCTGAGAGATGCGAGCTTGAATTTTCAGAGGAC	834
QY	1370	TTGGAAAGAAATATAAGTGGGATTTGGTAACCCCTTCAGGAGAAATATGGCTCGGAAATGA	1429
DB	833	TTGGAAAGAAATATAAGTGGGATTTGGTAACCCCTTCAGGAGAAATATGGCTCGGAAATGA	774
QY	1430	GTTTGTTTCGCAACTGACTTAATCAGCAACGCTATGTGCTTAAATACACCTTTAAAGACTG	1489
DB	773	GTTTGTTTCGCAACTGACTTAATCAGCAACGCTATGTGCTTAAATACACCTTTAAAGACTG	714
QY	1490	GGAAGGAATAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAA	1549
DB	713	GGAAGGAATAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAA	654
QY	1550	TTATAGGATTCACCTTTAAAGACTTACAGGGACAGCGGCAAAATAAGCAGCATCAGCCA	1609
DB	653	TTATAGGATTCACCTTTAAAGACTTACAGGGACAGCGGCAAAATAAGCAGCATCAGCCA	594
QY	1610	ACCAGGAATGATTTTAGCACAAGAGTGGAGACACGACAAATGATTTGCAAAATGTC	1669
DB	593	ACCAGGAATGATTTTAGCACAAGAGTGGAGACACGACAAATGATTTGCAAAATGTC	534
QY	1670	ACAAATGCTAACAGAGGCTGGTGGTTGATGATGCTGGTCTTCAACTTGAACGGAAAT	1729
DB	533	ACAAATGCTAACAGAGGCTGGTGGTTGATGATGCTGGTCTTCAACTTGAACGGAAAT	474
QY	1730	GTACTATCCACAGAGGCGAAGACACAAATAAGTTCAACGGCATTAATGGTACTACTGGAA	1789
DB	473	GTACTATCCACAGAGGCGAAGACACAAATAAGTTCAACGGCATTAATGGTACTACTGGAA	414
QY	1790	AGGCTCAGGCTATTCGCTCAAGGCCACACACCATGATGATCCGACGACAGATTTCTAAAC	1849
DB	413	AGGCTCAGGCTATTCGCTCAAGGCCACACACCATGATGATCCGACGACAGATTTCTAAAC	354
QY	1850	ATCCCAAGTCCAGTCAAGGACTGTCTGAACTATTTTCAAGACTTAAGCCAGTGCAT	1909
DB	353	ATCCCAAGTCCAGTCAAGGACTGTCTGAACTATTTTCAAGACTTAAGCCAGTGCAT	294
QY	1910	GAAAGTCAGGCTGGCGACTGTGTCTCTTCCACACAGAGGGCGTGTCTCGGTGCTGA	1969
DB	293	GAAAGTCAGG-TGGCGACTGTGTCTCTTCCACACAGAGGGCGTGTCTCGGTGCTGA	235
QY	1970	CGGACCCACATGCTCCAGATTAGAGCCCTGTAACCTTTATCACTTAAACTTGCACTCACTT	2029
DB	234	CGGACCCACATGCTCCAGATTAGAGCCCTGTAACCTTTATCACTTAAACTTGCACTCACTT	175
QY	2030	RACGACCAACAGACCCCTTAAACATCCATTAATTTGTGATTTAGACAGACACCTATGCA	2089
Db	174	RACGACCAACAAAGCAAGACCCCTTAAACATCCATTAATTTGTGATTTAGACAGACACCTATGCAA	115
QY	2090	AGATCAACCCGAGGCTGAGAAATCAGACTGACAGCTTTTACAGACGCTGCTGTCAACACCAAG	2149
Db	114	AGATCAACCCGAGGCTGAGAAATCAGACTGACAGCTTTTACAGACGCTGCTGTCAACACCAAG	55
QY	2150	AATGTTATGTGCAAGTGTATTCAGTAAA--TAACTGGAAAAACAGAACACTTATGT	2201
Db	54	AATGTTATGTGCAAGTGTATTCAGTAAA--TAACTGGAAAAACAGAACACTTATGT	1
RESULT 8			
BX348832		960 bp mRNA linear EST 08-APR-2004	
LOCUS		BX348832 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA	
DEFINITION		clone CS01037YG20 5-PRIME, mRNA sequence.	
ACCESSION		BX348832	
VERSION		BX348832.1 GI:30365305	
KEYWORDS		EST.	
SOURCE		Homo sapiens (human)	
ORGANISM		Homo sapiens	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE		1. (bases 1 to 960)	
AUTHORS		Li.W.B., Gruber,C., Jessee,J. and Polayes,D.	
TITLE		Full-length cDNA libraries and normalization	
JOURNAL		Unpublished (2001)	
COMMENT		Contact: Genoscope	
		Genoscope - Centre National de Sequencage	
		2 rue Gaston Crémieux, Cp 5706 - 91057 EVRY cedex - FRANCE	
		Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr	
		1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime	
		end enriched, double-strand cDNA was digested with Not I and cloned	
		into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library	
		was normalized. Library was constructed by Life Technologies, a	
		division of Invitrogen. This sequence belongs to sequence cluster	
		4496.r	
		For more information about this cluster, see	
		http://www.genoscope.cns.fr/cdna?e=CS0BAG030ZC09_CS02851_1&c=4496.r	
FEATURES		Location/Qualifiers	
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		/clone="CS01037YG20"	
		/tissue_type="PLACENTA COT 25-NORMALIZED"	
		/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"	
		/note="1st strand cDNA was primed with a NotI-oligo (dT)	
		primer. Five prime end enriched, double-strand cDNA was	
		digested with Not I and cloned into the Not I and EcoR V	
		sites of the pCMVSPORT 6 vector. Library was normalized."	
ORIGIN			
Query Match		36.8%; Score 840.6; DB 5; Length 960;	
Best Local Similarity		95.2%; Pred. No. 1.5e-220;	
Matches		916; Conservative 0; Mismatches 38; Indels 8; Gaps 5;	
QY	844	ACTCCCTCTCGACAAACAATTTGGAAAAACAGATTTTCGACGACGACGAGTAAATAACA	903
DB	5	ACATCCCTCTCGACAAACAATTTGGAAAAAC--GATTTTGGACGACGAGTAAATAACA	63
QY	904	AATTGCAAGATAAGAACAGTTCCTAGAAAAAGAGGTGCTAGCTATGGAAGACAGACACA	963
DB	64	AATTGCAAGATAAGAACAGTTCCTAGAAAAAGAGGTGCTAGCTATGGAAGACAGACACA	123
QY	964	TCATCCAACTCAGTCAATAAAAAAGAGAAAGATCAGCTACAGTGTAGTATCCAAAGC	1023
DB	124	TCATCCAACTCAGTCAATAAAAAAGAGAAAGATCAGCTACAGTGTAGTATCCAAAGC	183
QY	1024	AAAAATCCATCATTCAGAACTAGAAAAAAAATAAGTAGCTGCCACGCTGAATATTCAG	1083
DB	184	AAAAATCCATCATTCAGAACTAGAAAAAAAATAAGTAGCTGCCACGCTGAATATTCAG	243


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Db 271 |||||CATGGAGACAGTTAATAAATCTACTGATGATGTCACATCAAATCT---CTAAGGACCC 215
Qy 1169 CACTGTTGCTAAAGAGAGAAACAATCAGCTTCAGAGACTGCTGTAAGTATTCAAATCAGG 1228
Db 214 CACTGTTGCTAAAGAGAGAAACAATCAGCTTCAGAGACTGCTGTAAGTATTCAAATCAGG 155
Qy 1229 ACACACCACAAATGGCATCTACACGTTAAACATTTCCCTAAATTTCTACAGAAGAGATCAAGGC 1288
Db 154 ACACACCACGAATGGCATCTACACGTTAAACATTTCCCTAAATTTCTACAGAAGAGATCAAGGC 95
Qy 1289 CTACTGTGACATGGAAGCTGGAGGAGCGGTGGACAATTTATTCAGCGACGTGAGGATGG 1348
Db 94 CTACTGTGACATGGAAGCTGGAGGAGCGGTGGACAATTTATTCAGCGACGTGAGGATGG 35
Qy 1349 CAGCGTTGATTTTCAGAGGACTTGGAAAGAAATATA 1383
Db 34 CAGCGTT-ATTTTCAGAGGACGTGAAAGAAATAA 1

RESULT 10
AY407059
LOCUS 1213 bp DNA linear GSS 15-DEC-2003
DEFINITION Pan troglodytes ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence,
genomic survey sequence.
ACCESSION AY407059
VERSION AY407059.1 GI:39763030
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 (bases 1 to 1213)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
2 (bases 1 to 1213)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,
Todd,M.A., Tanenbaum,D.M., Civallo,D.R., Lu,F., Murphy,B.,
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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source Location/Qualifiers
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/locus_tag="HCM2764"

gene
ORIGIN
Query Match 35.0%; Score 798.8; DB 9; Length 1213;
Best Local Similarity 83.8%; Pred. No. 5.8e-209;
Matches 815; Conservative 0; Mismatches 158; Indels 0; Gaps 0;
Qy 873 CAGATTTTGGACGACGACAGTGAATAAACAATTCGAAGATGAAGAACAGTTTCTAGAA 932
Db 241 CAAGTCTGGAGAACATCATCTGGAAGAACACACTCAGTGGCTAATGAAGAGTTTCTAGAA 300
Qy 933 AAGAGGTGCTAGCTATGGAAGACAGCACATCATCACTCAGTCAATAAAGAGAG 992
Db 301 AAGAGGTGCTAGCTATGGAAGACAGCACATCATCACTCAGTCAATAAAGAGAG 360
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Qy 993 AAAGATCAGCTACAGTGTAGTATCCAGCAAAATTCATCATTGAAGAACTAGAAAAA 1052
Db 361 AAAGATCAGCTACAGTGTAGTATCCAGCAAAATTCATCATTGAAGAACTAGAAAAA 420
Qy 1053 AAAATAGTACCTGCCACGCTGAATAATTCAGTTCCTTCAAAGCAGCAACATGATCTCATG 1112
Db 421 AAAATAGTACCTGCCACGCTGAATAATTCAGTTCCTTCAAAGCAGCAACATGATCTCATG 480
Qy 1113 GAGACAGTTTAATAAATCTTACTGACTATGATGTCCACATCAAATCAGCTAAGGACCCCACT 1172
Db 481 GAGACAGTTTAATAAATCTTACTGACTATGATGTCCACATCAAATCAGCTAAGGACCCCACT 540
Qy 1173 GTTGTAAAGAGAAACAAATCAGCTTCAGAGACTGTGCTGAAAGTATTCAAATCAGGACAC 1232
Db 541 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 600
Qy 1233 ACCACAAATGGCATCTACACGTTAAATTCCTTAATTTCTACAGAAGATCAAGGCTTAC 1292
Db 601 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 660
Qy 1293 TGTGACATGGAAGCTGGAGGAGCGGTGGACAAATTTATTCAGCGACGTGAGGATGGCAGC 1352
Db 661 TGTGACATGGAAGCTGGAGGAGCGGTGGACAAATTTATTCAGCGACGTGAGGATGGCAGC 720
Qy 1353 GTTGATTTTCAGAGACTTGGAAAGAAATATAAAGTGGGATTTGGTAAACCCCTTCAGAGAA 1412
Db 721 GTTGATTTTCAGAGACTTGGAAAGAAATATAAAGTGGGATTTGGTAAACCCCTTCAGAGAA 780
Qy 1413 TATTGCTGGGAAATGAGTTTGTTCGCAACTGACTAATCAGCAACGCTATGTGCTTAA 1472
Db 781 TATTGCTGGGAAATGAGTTTGTTCGCAACTGACTAATCAGCAACGCTATGTGCTTAA 840
Qy 1473 ATACACCTTTAAAGACTTGGGAAGGAATGAGGCTTACTCATTTGTAACAATTTCTATCTC 1532
Db 841 ATACACCTTTAAAGACTTGGGAAGGAATGAGGCTTACTCATTTGTAACAATTTCTATCTC 900
Qy 1533 TCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGACTTACAGGGACAGCCGCAAA 1592
Db 901 TCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGACTTACAGGGACAGCCGCAAA 960
Qy 1593 ATAAGCAGCATCAGCAACCAAGGAATGATTTTACACAAGGATGGAGACACGACAA 1652
Db 961 ATAAGCAGCATCAGCAACCAAGGAATGATTTTACACAAGGATGGAGACACGACAA 1020
Qy 1653 TGTATTGCAAAATGTTCAAAATGCTTAACAGAGGCTGGTGGTTTGTGATGATGATGCTCT 1712
Db 1021 TGTATTGCAAAATGTTCAAAATGCTTAACAGAGGCTGGTGGTTTGTGATGATGATGCTCT 1080
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Db 1081 TCCAACTTGAACGGAATGTACTATCCACAAAGGCGAGAACACAAATAGTTTCAACGGCAT 1140
Qy 1773 AAATGGTACTACTGAAAGGCTCAGGCTATTCGCTCAAGGCCACCAACCATGATGATCGA 1832
Db 1141 AAATGGTACTACTGAAAGGCTCAGGCTATTCGCTCAAGGCCACCAACCATGATGATCGA 1200
Qy 1833 CCAGCAGATTTCT 1845
Db 1201 CCAGCAGATTTCT 1213

RESULT 11
CB528341/c
LOCUS 721 bp mRNA linear EST 05-AUG-2004
DEFINITION UI-H-FT2-bjg-j-05-0-UI-s1 NCI_CGAP_F72 Homo sapiens cDNA clone
ACCESSION UI-H-FT2-bjg-j-05-0-UI-3', mRNA sequence.
VERSION CB528341
KEYWORDS CB528341.1 GI:29387926
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
```

REFERENCE 1 (bases 1 to 721)
TITLE NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Dr. Gary W. Hunninghake, U of I
cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
<http://genome.uiowa.edu/distribution/cgap.html>
Seq primer: M13 FORWARD
POLYA=Yes.

FEATURES
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FT2"
/notes="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP FT2 is a subcloned cDNA library constructed from a pool of 81 RNA samples from Alveolar Macrophages challenged with different treatments. The mRNA samples were a mixture of these conditions (times refer to incubations following isolation by bronchoalveolar lavage) (some normal donor macrophages were cultured in some of the conditions, other donor macrophages in different conditions). The mRNA samples were pooled for library construction. Control 0 hours; control 3 hours; control 24 hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours; PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral vector (Ad5 CMV eGFP), moi 500, 3 hours; wt Adenoviral vector (Ad5 CMV eGFP), moi 500, 24 hours; wt Adenovirus moi 500, 3 hours; wt Adenovirus moi 500, 24 hours; Ad vector + LPS 3 hours; Ad vector + LPS 24 hours; wt Adenovirus + LPS 3 hours; wt Adenovirus + LPS 24 hours. The library was subcloned according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. The tissue was provided by Dr. Gary W. Hunninghake of the University of Iowa.
TAG TISSUE=Human Lung Alveolar Macrophage
TAG_LIB=UI-H-FT2
TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match 29.6%; Score 675.8; DB 6; Length 721;
Best Local Similarity 99.7%; Pred. No. 5e-175;
Matches 677; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1604 CAGCCAAACGAGAAATGATTTTACCAAGAGTGGAGACAAACGACAAATGATTTGCAA 1663
Db 721 CAGCCAAACGAGAAATGATTTTACCAAGAGTGGAGACAAACGACAAATGATTTGCAA 662

Qy 1664 ATGTTCAAAATGCTAACAGAGGCTGGTGGTTTGTGATGTCATGGTCTTCCAACTTGAA 1723
Db 661 ATGTTCAAAATGCTAACAGAGGCTGGTGGTTTGTGATGTCATGGTCTTCCAACTTGAA 602

Qy 1724 CGGAATGACTATCCACAGAGCGAGACACAAATAAGTTCAACGGCATTAATGGTACTA 1783
Db 601 CGGAATGACTATCCACAGAGCGAGACACAAATAAGTTCAACGGCATTAATGGTACTA 542

Qy 1784 CTGGAAGAGGCTCAGGCTATTTCGCTCAAGGCCACCAACCATGATGATCCGACGAGATTT 1843
Db 541 CTGGAAGAGGCTCAGGCTATTTCGCTCAAGGCCACCAACCATGATGATCCGACGAGATTT 482

Qy 1844 CTAAACATCCAGTCCACTGAGGAACTGTCTCGAATATTTTCAAGAACTTAAGCCAG 1903
Db 481 CTAAACATCCAGTCCACTGAGGAACTGTCTCGAATATTTTCAAGAACTTAAGCCAG 422

Qy 1904 TGCACCTGAAAGTACCGGCTGCGCACTGTCTCTTCCACACAGAGGCGGTGTGCTCGG 1963
Db 421 TGCACCTGAAAGTACCGGCTGCGCACTGTCTCTTCCACACAGAGGCGGTGTGCTCGG 362

Qy 1964 TGTGACGGGACCCACATCTCTCAGATTAGAGCTGTAACTTATCATTAACTTGCA 2023
Db 361 TGTGACGGGACCCACATCTCTCAGATTAGAGCTGTAACTTATCATTAACTTGCA 302

Qy 2024 TCACTTTAACGGACCAAGCAAGCCCTAAACATCCATAATTTGTGATTAGACAGACACCT 2083
Db 301 TCACTTTAACGGACCAAGCAAGCCCTAAACATCCATAATTTGTGATTAGACAGACACCT 242

Qy 2084 ATGCAAGATGAACCCGAGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCA 2143
Db 241 ATGCAAGATGAACCCGAGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCA 182

Qy 2144 ACCAAGAATGTTATGTGCAAGTTTATCAGTAATAAATCTGAAACAGAACACTTATGTTA 2203
Db 181 ACCAAGAATGTTATGTGCAAGTTTATCAGTAATAAATCTGAAACAGAACACTTATGTTA 122

Qy 2204 TACAATACAGATCATCTTGGAACTGCAATCTTCTGAGCACTGTTTATACACTGTGTAAT 2263
Db 121 TACAATACAGATCATCTTGGAACTGCAATCTTCTGAGCACTGTTTATACACTGTGTAAT 62

Qy 2264 ACCATATGTCCTGAATTC 2282
Db 61 ACCATATGTCCTGAATTC 43

RESULT 12
LOCUS AI862415 735 bp mRNA linear EST 26-AUG-1999
DEFINITION td16b10.x1 NCI CGAP Col6 Homo sapiens cDNA clone IMAGE:2075803 3', similar to TR:O15123 O15123 ANGIOPOIETIN-2, ; mRNA sequence.

VERSION AI862415
EST. AI862415.1 GI:5526522
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 735)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone Distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -400P from Gibco
High quality sequence stop: 475.
Location/Qualifiers
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/clone_lib="NCI CGAP Col6"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site 1: Not I; Site 2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP Col10 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDs 1057416-1061255, and 1144584-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

```
Query Match      29.1%; Score 663.4; DB 1; Length 735;
Best Local Similarity 97.4%; Pred. No. 1.3e-171;
Matches 684; Conservative 0; Mismatches 17; Indels 1; Gaps 1;

QY 1581 ACAGCGCGCAAAATTAAGCAGCATCAGCCAAACAGAGAAATGATTTAGCAACAAGATGGA 1640
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 735 ACAGCGCGCAAAATTAAGCAGCATCAGCCAAACAGAGAAATGATTTAGCAACAAGATGGA 676

QY 1641 GACACGCAAAATGATTTGCAAAATGTTCCAAATGCTTAACAGGAGGCTGGTGGTTGAT 1700
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 675 GACAAAGCAAAATAGTATTTGCAAAATGTTCCAAATGCTTAACAGGAGGCTGGTGGTTGAT 616

QY 1701 GCATGTGTCCTTCCAACTTGAACGGAATGTTACTATCCACAGGAGGAGCAACAATTAAG 1760
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 615 GCATGTGTCCTTCCAACTTGAACGGAATGTTACTATCCACAGGAGGAGCAACAATTAAG 557

QY 1761 TTCAACGGGCAATTAATGTTACTTACGAAAGGCTCAGGCTATTCGCTCAAGGCCCAAC 1820
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 556 TTCAACGGGCAATTAATGTTACTTACGAAAGGCTCAGGCTATTCGCTCAAGGCCCAAC 497

QY 1821 ATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGGAACTGTCTCGAAC 1880
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 496 ATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGGAACTGTCTCGAAC 437

QY 1881 TATTTTCAAGACTTAAGCCAGTGCATGAAAGTCAAGGCTGCCACTGTCTCTCTTC 1940
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 436 TATTTTCAAGACTTAAGCCAGTGCATGAAAGTCAAGGCTGCCACTGTCTCTCTTC 377

QY 1941 CACCACAGAGGCGGTGTGTCGGTGTCTGACGGAGCCCAATGCTCCAGATTAGAGCCCTGT 2000
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 376 CACCACAGAGGCGGTGTGTCGGTGTCTGACGGAGCCCAATGCTCCAGATTAGAGCCCTGT 317

QY 2001 AAACHTTATCACTTAACTTGTGATCACTTAAACGAGACCAAGCAAGACCCCTAAACATCCAT 2060
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 316 AAACHTTATCACTTAACTTGTGATCACTTAAACGAGACCAAGCAAGACCCCTAAACATCCAT 257

QY 2061 AATTGTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGAGAACTCAGACTGCAC 2120
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 256 AATTGTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGAGAACTCAGACTGCAC 197

QY 2121 AGTTTACAGAGCTGTGTCAACCAAGAAATGTTATGTGCAAGTATTATCAGTAATAAATAC 2180
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 196 AGTTTACAGAGCTGTGTCAACCAAGAAATGTTATGTGCAAGTATTATCAGTAATAAATAC 137

QY 2181 TGGAAAACAGAACACTTATGTTATCAATACAGATCATCTTGGAACTGCAATCTTCTGAG 2240
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 136 TGGAAAACAGAACACTTATGTTATCAATACAGATCATCTTGGAACTGCAATCTTCTGAG 77

QY 2241 CACTGTTTATACACTGTGTAATACCCATATCTCTCTGAAATC 2282
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 76 CACTGTTTATACACTGTGTAATACCCATATCTCTCTGAAATC 35
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RESULT 13
BG714406
LOCUS BG714406 696 bp mRNA linear EST 08-MAY-2001
DEFINITION 602669330F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:4792831 5',
mRNA sequence.
ACCESSION BG714406
VERSION BG714406.1 GI:13993337
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 696)
NIH-MGC <http://mgs.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLNL0671 row: k column: 08
High quality sequence stop: 677.

FEATURES
source

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1..696
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792831"
/tissue_type="hypothalamus"
/lab_host="DH10B"
/clone_lib="NIH_MGC_96"
/notes="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site1: BamHI; Site2: SalI-XhoI  
(gtcgag); Oligo-dr primed using primer  
5'-TTTTTTTATTTTNN-3', size-selected for average  
insert size 2.3 kb and normalized to ROT 5. This is a  
primary library enriched for full-length clones and  
constructed using the Cap-trapper method (Carninci, in  
preparation). Library constructed by M. Brownstein  
(NIH/NHGRI, National Institutes of Health). Note: this is  
a NIH_MGC Library."
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ORIGIN

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Query Match      28.6%; Score 652.8; DB 4; Length 696;
Best Local Similarity 98.7%; Pred. No. 1.1e-168;
Matches 679; Conservative 0; Mismatches 7; Indels 2; Gaps 2;

QY 162 TTACTGCATGCTGGAGAGAACACAGCAGTAGTAAAAACAGGTTTGTCTACTGAAAAAGAGG 221
DB 8 TTACTGCATGCTGGAGAGAACACAGCAGTAGTAAAAACAGGTTTGTCTACTGAAAAAGAGG 67

QY 222 AAAGAGAAGACTTTCATTGACGGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTTCAGA 281
DB 68 AAAGAGAAGACTTTCATTGACGGACCCAGCCATGGCAGCGTAGCAGCCCTCGGTTTCAGA 127

QY 282 CGGACAGAGCTCGGAGACTCTGGACGTGTGTTTGCCTCAAGTTTGTCTAAGCTGCTGGTTT 341
DB 128 CGGACAGAGCTCGGAGACTCTGGACGTGTGTTTGCCTCAAGTTTGTCTAAGCTGCTGGTTT 187

QY 342 ATTAAGTGAAGAAAGATGTGGCAGATGTTTTCCTTACTCTGAGCTGTGATCTTGTCTTG 401
DB 188 ATTAAGTGAAGAAAGATGTGGCAGATGTTTTCCTTACTCTGAGCTGTGATCTTGTCTTG 247

QY 402 GCCGAGGCTTAACAACCTTTCCGAGAGCATGGACAGCATAGGAAAGCAAGCAATATCAG 461
DB 248 GCCGAGGCTTAACAACCTTTCCGAGAGCATGGACAGCATAGGAAAGCAAGCAATATCAG 307

QY 462 GTCCAGCATGGGTCTCTGAGCTACACTTTCCTCTCCGAGAGATGGACAACTGCCGCTCT 521
DB 308 GTCCAGCATGGGTCTCTGAGCTACACTTTCCTCTCCGAGAGATGGACAACTGCCGCTCT 367

QY 522 TCCTCCAGCCCCCTACGTGTCCAATGTGTGAGAGGAGCGCCGCTCGAATACGATGAC 581
DB 368 TCCTCCAGCCCCCTACGTGTCCAATGTGTGAGAGGAGCGCCGCTCGAATACGATGAC 427

QY 582 TCAGTGCAGAGGCTGCAAGTCTCGAGAACATCATGGAACAAACACACACACACACACATG 641
DB ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Db      428 TCCTGTCAGAGGCTGCAAGTGTCTGGAGAACATCATGGAACAAACACTCAGTGGCTAATG 487
QY      642 AAGCTTTCAGAAATATATCCAGGACCAACATCAAGA-AAGAAATGGTAGAGATACAGCAGA- 699
Db      488 AAGCTTTCAGAAATATATCCAGGACCAACATCAAGAAGAAATGGTAGAGATACAGCAGAC 547
QY      700 ATGCACTAGAGAACCCAGACGGCTGTGATGTAGATAGAAATAGGAGCAAAACCTGTTGAACCAA 759
Db      548 ATGCACTAGAGAACCCAGACGGCTGTGATGTAGATAGAAATAGGAGCAAAACCTGTTGAACCAA 607
QY      760 CAGCTGAGCAAAACCGGAGCTTAACTGATGTGAGCCCAAGTATTAAATCAGACCAACGA 819
Db      608 CAGCCGAGCAAAACCGGAGCTTAACTGATGTGAGCCCAAGTATTACATCAGAGCAGCA 667
QY      820 GACTTGAACCTTCAGCTCTTGGAAACACTC 847
Db      668 GACTTGAACCTTCAGCTCTTGGAAACACTC 695

RESULT 14
LOCUS   AY407060
DEFINITION Mus musculus ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407060
VERSION   AY407060.1 GI:39763031
KEYWORDS GSS.
SOURCE   Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,C., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE    Inferring nonneutral evolution from human-chimp-mouse orthologous gene trices
JOURNAL  Science 302 (5652), 1960-1963 (2003)
PUBMED   14671302
REFERENCE
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferreria,S., Wang,C., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
TITLE    Direct Submission
JOURNAL  Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT   This sequence was made by sequencing genomic exons and ordering them based on alignment.
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            /locus_tag="HGN2764"

gene
ORIGIN
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Best Local Similarity 78.2%; Pred. No. 3.5e-161;
Matches 765; Conservative 0; Mismatches 210; Indels 3; Gaps 1;

QY      873 CAGATTTTGGACCAAGACAGTGAATTAACAAATTGCAAGATGAAGACAGTTTCTAGAA 932
Db      241 CAGTGTCTGGAGACATCTTAGAGAACACACACAGTGGCTGATGAAGAGCTTCTTAGAA 300
QY      933 AAGAGGTGTAGTATGGAAGACAGCAGCATCATCTCACTACATCAATAAAGAGAG 992
Db      301 CAGAAAGTTCTGGATGGAGGGGCAAGCAGCAGCGAGCTACAGTCCATGAAGAGCAG 360
QY      993 AAGATCAGCTACAGTGTGTAGTATCCCAAGCAAAATTCATCATTTGAAGAACTAGAAAAA 1052

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Db      361 AAGGACGAGCTCCAGTGTCTGGTGTCCAAGCAGAGCTCTGTCTATTGACGAGCTGGAGAAG 420
QY      1053 AAAATAGTAGTACGCCACGGTGAATTAATTCAGTTCTTTCAAAGCAGCAACATGATCTCATG 1112
Db      421 AAGCTGGTGCACAGCCACGGTCAACAACTCGCTCCTTTCAAGAGCAGCAGCATGACCTAATG 480
QY      1113 GAGACAGTTTAATACTTACTGACTATGATGTCCACATCAAACTCAACTCAGCTAAGGACCC---C 1169
Db      481 GAGACCGTCAACAGAGCTTGTCTGACCATGATGTTCATCAACCCCACTCAGCCCAAGAGCTCGGTT 540
QY      1170 ACTGTTGCTAAAGAGAAACAAATCAGCTTCAGAGACTGTGCTGAAGTATTCAAATCAGGA 1229
Db      541 GCTATCCGTAAGAAGAGCAAAACCCCTTCAGAGACTGTGCGGAATTTCTCAAGTCAGGA 600
QY      1230 CACACCACAAATGGCACTCTACAGCTTTAACTCCCTTAATTTCTACAGAAGAGATCAAGGCC 1289
Db      601 CTCACCACAGTGGCATCTACACACTGACTCTCCCACTCCACACAGAGAGATCAAGGCC 660
QY      1290 TACTGTGACATGGAAGCTGGAGAGCGGGTGGACAATTAATTTCAGCGACGTGAGGATGGC 1349
Db      661 TACTGTGACATGGAAGCTGGAGAGCGGGTGGACAATTAATTTCAGCGACGTGAGGATGGC 720
QY      1350 AGCGTTGATTTTCAGAGGACTTGGAAAGAAATATAAAGTGGATTTGCTAACCCCTTCAGGA 1409
Db      721 AGTGTGGACTTCCAGAGGACGTGGAAAGAAATACAAAGAGGGCTTCGGAGCCCTCTGGGA 780
QY      1410 GAATATTGCTGGGAAATGAGTTGTTTTCGCAACTGACTAATCAGCAACCGCTATGTGCTT 1469
Db      781 GAGTACTGCTGGGCAATGAGTTTGTCTCCAGCTGACCGGTGAGCACCGCTACGTGCTT 840
QY      1470 AAAATACACTTAAAGACTGGGAAGGAAATGAGGCTTACTCATTTGATGAACAATTTCTAT 1529
Db      841 AAGATCCAGCTGAAGGACTGGGAAGGCAACGAGGCGCAATTCGGCTGTATGATCACTTCTAC 900
QY      1530 CTCTCAAGTGAAGAACTCAATTAATAGATTCACCTTAAGAGCTTACAGGAGACGACGGC 1589
Db      901 CTCGCTGGTGAAGAGTCCAACTACAGGATTCACCTTACAGGACTCAGGGGACCGCGGGC 960
QY      1590 AAAATAAGCAGACTCAGCCAAACAGGAAATGATTTTAGCAAAAGGATGAGACCAACGAC 1649
Db      961 AAAATAAGTAGCATCAGCCAAACAGGAGATGATTTTAGCAAAAGGATTCGGACATGAC 1020
QY      1650 AAATGATTTTGAATTTTTCACAAATGCTTAACAGGAGGCTGGTGGTTGATGATGATGCT 1709
Db      1021 AAATGATCTGCAAGTGTTCCTCCAGATGCTCTCAGGAGGCTGGTGGTTGACGATGCTGT 1080
QY      1710 CTTTCAACTTTGAACGGAATGATCTATCCACAGAGGAGCAACAAATTAAGTTCAAGCGC 1769
Db      1081 CTTTCAACTTTGAATGAGACAGTACTACCCCAAAAAACAGAAATCAATAAGTTTAAACGGT 1140
QY      1770 ATTAAATGTTACTTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCCAACCATGATGATC 1829
Db      1141 ATCAAGTGGTACTTACTTGGAAAGGGGTTCGGCTACTTCGCTCAAGGCCCAACCATGATGATC 1200
QY      1830 CGACACGACAGATTCTTAA 1847
Db      1201 CGGCCAGCAGATTCTTAA 1218

RESULT 15
LOCUS   AI809922/c
DEFINITION AI809922 647 bp mRNA linear EST 19-DEC-1999
            wf59g08.x1 Soares_NFL.T.GBC.S1.Homo sapiens cDNA clone
            IMAGE:2359934 3' similar to TR:077802 077802 ANGIOPOIETIN-2 ;, mRNA
            sequence.
ACCESSION AI809922
VERSION   AI809922.1 GI:5396488
KEYWORDS Homo sapiens (human)
SOURCE    Homo sapiens
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE 1 (bases 1 to 647)
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 1180 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 455.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:235934"
/lab_host="DH10B"
/clone_lib="Soares NFL T GBC S1"
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
a modified polylinker; Site 1: Not 1; Site 2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCI CGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo. "

Query Match 26.8%; Score 611.8; DB 1; Length 647;
Best Local Similarity 99.7%; Pred. No. 2.4e-157;
Matches 613; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1668 TCACAAATGCTAACAGGAGGCTGGTGGTTTGATGATGATGGTCTTCCAACTTGAACGGA 1727
Db 647 TCACAAATGCTAACAGGAGGCTGGTGGTTTGATGATGATGGTCTTCCAACTTGAACGGA 588
QY 1728 ATGTACTATCCACAGGCGAGAACCAATAAGTTCAACGGCATTAATGGTACTACTGG 1787
Db 587 ATGTACTATCCACAGGCGAGAACCAATAAGTTCAACGGCATTAATGGTACTACTGG 528
QY 1788 AAAGGCTCAGGCTATTCGGCTCAAGGCCCAACCATGATGATCCGACCGAGATTCTTAA 1847
Db 527 AAAGGCTCAGGCTATTCGGCTCAAGGCCCAACCATGATGATCCGACCGAGATTCTTAA 468
QY 1848 ACATCCAGTCCACCTGAGGAACCTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCA 1907
Db 467 ACATCCAGTCCACATGAGGAACCTGTCTCGAACTATTTTCAAGACTTAAAGCCAGTGCA 408
QY 1908 CTGAAAGTCAACGGCTGCGCACTGTGTCTTCCACCAAGAGGGCGTGTCTCGGTGCT 1967
Db 407 CTGAAAGTCAACGGCTGCGCACTGTGTCTTCCACCAAGAGGGCGTGTCTCGGTGCT 348
QY 1968 GACGGGACCCATGCTCCAGATTAGAGCTGTAACTTTATCACTTAACTTGCATCAC 2027
Db 347 GACGGGACCCATGCTCCAGATTAGAGCTGTAACTTTATCACTTAACTTGCATCAC 288
QY 2028 TTAAACGACCAAGCAAGACCCCTAAACATCCATATTTGATTAGACAGAACACCTATGC 2087
Db 287 TTAAACGACCAAGCAAGACCCCTAAACATCCATATTTGATTAGACAGAACACCTATGC 228
QY 2088 AAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGCGTGTGTCAACCA 2147
Db 227 AAAGATGAACCCGAGGCTGAGAAATCAGACTGACAGTTTACAGCGTGTGTCAACCA 168
QY 2148 AGAATGTTATGTGCAAGTTTATCAGTTAAATACTGGAACACAGACACTTATGTTATCA 2207
Db 167 AGAATGTTATGTGCAAGTTTATCAGTTAAATACTGGAACACAGACACTTATGTTATCA 108

QY 2208 ATACAGATCATCTTGGAACTGCAATTCCTTCTGAGCACTGTTTATACACTGTGTAAATACCC 2267
Db 107 ATACAGATCATCTTGGAACTGCAATTCCTTCTGAGCACTGTTTATACACTGTGTAAATACCC 48
QY 2268 ATATGCTCTGAATTC 2282
Db 47 ATATGCTCTGAATTC 33
Search completed: July 29, 2005, 09:49:48
Job time : 8071.43 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 02:51:04 ; Search time 2039.78 Seconds
(without alignments)
7240.933 Million cell updates/sec

Title: US-10-603-293-5
Perfect score: 2282
Sequence: 1 gaattcctgggttggttt.....taccatgatgctgaattc 2282

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7287783 seqs, 3236178273 residues

Total number of hits satisfying chosen parameters: 14575566

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA:
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2: /cgn2_6/prodata/1/pubpna/PCT_NEW_PUB.seq:
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25: /cgn2_6/prodata/1/pubpna/US60_NEW_PUB.seq:
26: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2282	100.0	2282	14	US-10-186-817-5 Sequence 5, Appli
3	2282	100.0	2282	14	US-10-225-060-5 Sequence 5, Appli
4	2282	100.0	2282	15	US-10-321-332-5 Sequence 5, Appli
5	2282	100.0	2282	16	US-10-719-615-5 Sequence 5, Appli
6	2282	100.0	2282	16	US-10-179-820-5 Sequence 5, Appli
7	2282	100.0	2282	21	US-10-603-293-5 Sequence 5, Appli

US-10-179-744-5

Sequence 5, Appli

US-09-998-833-3

Sequence 3, Appli

US-10-101-510-460

Sequence 3, Appli

US-10-373-561-3

Sequence 3, Appli

US-10-317-803-18

Sequence 18, Appli

US-10-789-222-33

Sequence 33, Appli

US-10-827-759A-2

Sequence 2, Appli

US-10-988-245-3

Sequence 3, Appli

US-10-738-404-3

Sequence 3, Appli

US-10-712-124-103

Sequence 103, Appli

US-10-044-090-23

Sequence 23, Appli

US-10-133-013-250

Sequence 250, Appli

US-10-044-090-24

Sequence 24, Appli

US-10-317-803-21

Sequence 21, Appli

US-10-852-335A-56

Sequence 56, Appli

US-10-928-911-23

Sequence 23, Appli

US-10-928-911-23

Sequence 23, Appli

US-10-317-803-22

Sequence 22, Appli

US-10-827-759A-9

Sequence 9, Appli

US-09-832-355A-95

Sequence 95, Appli

US-10-225-060-21

Sequence 21, Appli

US-10-928-911-21

Sequence 21, Appli

US-09-832-355A-124

Sequence 124, Appli

US-10-317-803-11

Sequence 11, Appli

US-10-789-222-34

Sequence 34, Appli

US-10-827-759A-5

Sequence 5, Appli

US-10-764-420-1571

Sequence 1571, Appli

US-10-225-060-19

Sequence 19, Appli

US-10-928-911-19

Sequence 19, Appli

US-10-225-060-25

Sequence 25, Appli

US-10-928-911-25

Sequence 25, Appli

US-10-317-803-4

Sequence 4, Appli

US-09-790-289-1

Sequence 1, Appli

US-10-468-582-1

Sequence 1, Appli

US-11-028-971-1

Sequence 1, Appli

US-10-179-744-3

Sequence 3, Appli

US-10-186-817-3

Sequence 3, Appli

RESULT 1

US-10-179-744-5

Sequence 5, Application US/10179744

Publication No. US20020173627A1

GENERAL INFORMATION:

APPLICANT: Davis, Samuel et al.

TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF

FILE REFERENCE: REG 330-F-PCT-US

CURRENT APPLICATION NUMBER: US/10/179,744

CURRENT FILING DATE: 2002-06-24

PRIOR APPLICATION NUMBER: US/08/817,318

PRIOR FILING DATE: 1999-09-16

NUMBER OF SEQ ID NOS: 6

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 5

LENGTH: 2282

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Unknown Organism

FEATURE:

NAME/KEY: CDS

LOCATION: (357)...(1847)

US-10-179-744-5

Query Match 100.0%; Score 2282; DB 13; Length 2282;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY

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Qy	61	TCTGGGAGAGAGGAAACAAGGACCGGTGAAGCTGCTGTATAAGCTGCACAGACCCCTC	120
Db	61	TCTGGGAGAGAGGAAACAAGGACCGGTGAAGCTGCTGTATAAGCTGCACAGACCCCTC	120
Qy	121	CCAAAGTGAGCAGGACTGTCTTCCCTCAGCTGCAATCTGACAGTTTACTGCATGCTCGGAGAG	180
Db	121	CCAAAGTGAGCAGGACTGTCTTCCCTCAGCTGCAATCTGACAGTTTACTGCATGCTCGGAGAG	180
Qy	181	AACACAGCAGTAAAAACACAGTTTGTCTACTGGAATAAGAGAAAGAGAAAGACTTTCAATTG	240
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Qy	241	ACGGACCCAGCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGCGACAGCTCGGGACTC	300
Db	241	ACGGACCCAGCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGCGACAGCTCGGGACTC	300
Qy	301	TGGACGTGTGTTTGTCCCTCAAGTTTGCTAAGCTGCTGCTGTTTATTACTGGAAGAAGAAATGT	360
Db	301	TGGACGTGTGTTTGTCCCTCAAGTTTGCTAAGCTGCTGCTGTTTATTACTGGAAGAAGAAATGT	360
Qy	361	GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGCGACGCTATAACAAT	420
Db	361	GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGCGACGCTATAACAAT	420
Qy	421	TTCGGAAGAGCATGGACAGCATAGGAAGAGCAATATCAGGTCACAGCATGGGTCCTGCA	480
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Qy	481	GCTACACTTTCCTCCTGCCAGATGACAACTGCCCGCTCTTCTCCAGGCCCTTACGTGT	540
Db	481	GCTACACTTTCCTCCTGCCAGATGACAACTGCCCGCTCTTCTCCAGGCCCTTACGTGT	540
Qy	541	CCAATGCTGTGCAGAGGGAACGCGCGCTCGAATAACGATGATCGGTCGAGAGGCTGCAAG	600
Db	541	CCAATGCTGTGCAGAGGGAACGCGCGCTCGAATAACGATGATCGGTCGAGAGGCTGCAAG	600
Qy	601	TGCTGGAGAACATCATGGAAAAACAACACTCAGTGGCTTAATGAAGCTTGAAGTTATATCC	660
Db	601	TGCTGGAGAACATCATGGAAAAACAACACTCAGTGGCTTAATGAAGCTTGAAGTTATATCC	660
Qy	661	AGGACAACTCAAGAAAAAATGGTAGAGATACAGCAGAATGCAAGTACAGAACACAGACGG	720
Db	661	AGGACAACTCAAGAAAAAATGGTAGAGATACAGCAGAATGCAAGTACAGAACACAGACGG	720
Qy	721	CTGTGATGATAGAAAAATAGGACAAAACCTGTTGAAACAAAACAGCTGAGCAAAACGCGAAGT	780
Db	721	CTGTGATGATAGAAAAATAGGACAAAACCTGTTGAAACAAAACAGCTGAGCAAAACGCGAAGT	780
Qy	781	TAACTGATGTGGAGCCCAAGTATTAATCAGACCCAGACACTTGACCTTTCAGCTCTTGG	840
Db	781	TAACTGATGTGGAGCCCAAGTATTAATCAGACCCAGACACTTGACCTTTCAGCTCTTGG	840
Qy	841	AACACTCCCTCTCGACAAAACAAATTGGAAAAACAGATTTTGGACACAGACAGTGAATAA	900
Db	841	AACACTCCCTCTCGACAAAACAAATTGGAAAAACAGATTTTGGACACAGACAGTGAATAA	900
Qy	901	ACAAAATTGCAAGATAAGAACAGTTTCTAGAAAAGAGGTGCTAGCTATGGAAGACAAAGC	960
Db	901	ACAAAATTGCAAGATAAGAACAGTTTCTAGAAAAGAGGTGCTAGCTATGGAAGACAAAGC	960
Qy	961	ACATCATCCAACCTACAGTCAATAAAGACAGAAAGATCAGCTACAGGCTTTAGTATCCA	1020
Db	961	ACATCATCCAACCTACAGTCAATAAAGACAGAAAGATCAGCTACAGGCTTTAGTATCCA	1020
Qy	1021	AGCAAAATCCATCATTGAAAGAACTGAAAAAAAATAGTGACTGCCACCGGTGAATAATT	1080
Db	1021	AGCAAAATCCATCATTGAAAGAACTGAAAAAAAATAGTGACTGCCACCGGTGAATAATT	1080
Qy	1081	CAGTTCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTTAATACTTACTCACTATGA	1140

Db	1081	CAGTTCCTTCAAAAGCAGCAACATGATCTCATGGAGACAGTTAATAACTTACTGACTA	1141
Qy	1141	TGTCACATCAAACTCAGCTAAGACCCCACTGTTGCTAAAGAGAAACAATCAGCTTCA	1200
Db	1141	TGTCACATCAAACTCAGCTAAGACCCCACTGTTGCTAAAGAGAAACAATCAGCTTCA	1200
Qy	1201	GAGACTGTGCTGAAGTATTCAAAATCAGGACACACCACCAATGGCATCTACACGTTAACAT	1260
Db	1201	GAGACTGTGCTGAAGTATTCAAAATCAGGACACACCACCAATGGCATCTACACGTTAACAT	1260
Qy	1261	TCCCTAATTTCTACAGAAGATCAAGGCCCTACTGTGTGACATGGAAAGCTGGAGGAGCGGGT	1320
Db	1261	TCCCTAATTTCTACAGAAGATCAAGGCCCTACTGTGTGACATGGAAAGCTGGAGGAGCGGGT	1320
Qy	1321	GGACAAATTTATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGGACTTTGAAAGAAAT	1380
Db	1321	GGACAAATTTATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGGACTTTGAAAGAAAT	1380
Qy	1381	ATAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTTTCGC	1440
Db	1381	ATAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTTTCGC	1440
Qy	1441	AACGTGACTAATCAGCAACGCTATGTGCTTAAANAATACACTTAAAGACTGGGAAGGGAATG	1500
Db	1441	AACGTGACTAATCAGCAACGCTATGTGCTTAAANAATACACTTAAAGACTGGGAAGGGAATG	1500
Qy	1501	AGGCTTACTCATTTGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATTTATAGGATTC	1560
Db	1501	AGGCTTACTCATTTGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATTTATAGGATTC	1560
Qy	1561	ACCTTAAAGGACTTACAGGGACAGCCGGCAAAAATAAGCAGCATCAGCCAAACGAGGAAATG	1620
Db	1561	ACCTTAAAGGACTTACAGGGACAGCCGGCAAAAATAAGCAGCATCAGCCAAACGAGGAAATG	1620
Qy	1621	ATTTTACCAAAAGGATGGAGACAAAGAAATGTTATTTGCAAAATGTTCAAAATGCTTAA	1680
Db	1621	ATTTTACCAAAAGGATGGAGACAAAGAAATGTTATTTGCAAAATGTTCAAAATGCTTAA	1680
Qy	1681	CAGGAGCTCGTGGTTTGATGCAATGGTGCTTCCAACTTTGAACGGAATGTACTATCCAC	1740
Db	1681	CAGGAGCTCGTGGTTTGATGCAATGGTGCTTCCAACTTTGAACGGAATGTACTATCCAC	1740
Qy	1741	AGAGGCGAGAACAAAAATAGTTTCAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCT	1800
Db	1741	AGAGGCGAGAACAAAAATAGTTTCAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCT	1800
Qy	1801	ATTTCGCTCAGGGCCACAAACATGATTCGACACAGAGATTTCTTAAACATCCAGTCCA	1860
Db	1801	ATTTCGCTCAGGGCCACAAACATGATTCGACACAGAGATTTCTTAAACATCCAGTCCA	1860
Qy	1861	CCTGAGGAATGTCGAACTATTTTCAAGACTTAAGCCCACTGACATGAAAGTCACCG	1920
Db	1861	CCTGAGGAATGTCGAACTATTTTCAAGACTTAAGCCCACTGACATGAAAGTCACCG	1920
Qy	1921	CTCGCACTGTGCTCTTCCACCAAGAGGGCGTGTGCTCGTGTGTCAGCGGACCCACA	1980
Db	1921	CTCGCACTGTGCTCTTCCACCAAGAGGGCGTGTGCTCGTGTGTCAGCGGACCCACA	1980
Qy	1981	TGCTCAGATTAGAGCTGTAAACTTTTATCACTTAACTTGCATCTTAAACGGAACAAA	2040
Db	1981	TGCTCAGATTAGAGCTGTAAACTTTTATCACTTAACTTGCATCTTAAACGGAACAAA	2040
Qy	2041	GCAAGCCCTTAAACATCCATTAATTTGATTTAGACAGAACACCTATCGAAGATGAACCCG	2100
Db	2041	GCAAGCCCTTAAACATCCATTAATTTGATTTAGACAGAACACCTATCGAAGATGAACCCG	2100
Qy	2101	AGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAGAAATGTTATG	2160
Db	2101	AGGCTGAGAAATCAGACTGACAGTTTACAGACGCTGCTGTCAACAACCAAGAAATGTTATG	2160
Qy	2161	CAAGTTTATCAGTAAATAACTGGAACAGAACACTTATGTTTATACAAATACAGATCATCT	2220
Db	2161	CAAGTTTATCAGTAAATAACTGGAACAGAACACTTATGTTTATACAAATACAGATCATCT	2220

QY 2221 TGGAACTGCAATCTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCTGAAT 2280
Db 2221 TGGAACTGCAATCTCTGAGCACTGTTTATACACTGTGTAAATACCCATATGTCCTGAAT 2280
QY 2281 TC 2282
Db 2281 TC 2282
RESULT 2
US-10-186-817-5
; Sequence 5, Application US/10186817
; Publication No. US20030040463A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: Tie-2 Ligands, Methods of Making and Uses Thereof
; FILE REFERENCE: REG 330-G-PCT-US
; CURRENT APPLICATION NUMBER: US/10/186,817
; PRIOR FILING DATE: 2002-07-01
; APPLICATION NUMBER: US/08/930,721
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: PCT/US96/04806
; PRIOR FILING DATE: 1996-04-05
; PRIOR APPLICATION NUMBER: PCT/US95/12935
; PRIOR FILING DATE: 1995-10-06
; PRIOR APPLICATION NUMBER: 08/418,595
; PRIOR FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (357)..(1844)
US-10-186-817-5
Query Match 100.0%; Score 2282; DB 14; Length 2282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 61 TCTGGGAGAGAGAAACAAGGACCGTGAAGCTGCTCTGTAAAGCTGACACAGCCCTC 120
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Db 121 CCAAGTCAGCAGGACTGTTCTTCCACTGCAATCTGACAGTTTACTGATCGCTGGAGAG 180
QY 181 AACACAGCAGTAAACACAGCTTTGCTACTGGAAGAGAGAGAAAGAGAACTTTCATTG 240
Db 181 AACACAGCAGTAAACACAGCTTTGCTACTGGAAGAGAGAGAAAGAGAACTTTCATTG 240
QY 241 ACGACCCAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGACTC 300
Db 241 ACGACCCAGCCATGGCAGCGTAGCAGCCCTGCGTTTCAGACGGCAGCAGCTCGGACTC 300
QY 301 TGGACGTGTGTTGCCCTCAAGTTTGTAGCTGCTGTTTATTACTGAAGAAAGATGT 360
Db 301 TGGACGTGTGTTGCCCTCAAGTTTGTAGCTGCTGTTTATTACTGAAGAAAGATGT 360
QY 361 GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTGGCCGCGACCTTATACAACT 420
Db 361 GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTGGCCGCGACCTTATACAACT 420
QY 421 TTCGGAAGAGCATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCTGCA 480

Db 421 TTCGGAAGAGCATGGACAGCATAGGAAGAGCAATATCAGGTCCAGCATGGGTCTCTGCA 480
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Db 481 GCTACACTTTCCTCTGCGCAGAGATGGACAACTGCGCGCTTCTCTCCAGCCCTTACGTGT 540
QY 541 CCAATGCTGTGAGAGGGAGCGCGCTCGAATACGATGACTCGGTGCGAGAGCTGCAAG 600
Db 541 CCAATGCTGTGAGAGGGAGCGCGCTCGAATACGATGACTCGGTGCGAGAGCTGCAAG 600
QY 601 TGCTGAGAACATCATGGAACCAACACACTCAGTGGCTTAATGAAGCTTGAGAATATATCC 660
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Db 1621 ATTTAGCAAAAGATGAGACAACGACAAATATTTGCAAAATGTTACAAATGCTTAA 1680
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QY 2161 CAAAGTTATCAGTAATTAACCTGGAACAGAACACTTATGTTATACAATACAGATCATCT 2220
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QY 2281 TC 2282
Db 2281 TC 2282
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RESULT 3
US-10-225-060-5
; Sequence 5, Application US/10225060
; Publication No. US20030092891A1
; GENERAL INFORMATION:
; APPLICANT: Davis et al.
; TITLE OF INVENTION: Expressed Ligand - Vascular Intercellular Signaling
; FILE OF INVENTION: Molecule
; FILE REFERENCE: REG 333-Z
; CURRENT APPLICATION NUMBER: US/10/225,060
; CURRENT FILING DATE: 2002-08-21
; PRIOR APPLICATION NUMBER: US/09/709,188
; PRIOR FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 08/740,223
; PRIOR FILING DATE: 1996-10-25
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 2282
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (357)..(1844)
; OTHER INFORMATION:
US-10-225-060-5
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Query Match 100.0%; Score 2282; DB 14; Length 2282;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2221 TGGAACTGCATTTCTTGAGCACTGTTTATACACTGTGTAAATACCCATATGCTCTGAAT 2280
Qy 2281 TC 2282
Db 2281 TC 2282
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US-10-179-820-5
; Sequence 5, Application US/10179820
; Publication No. US20030166858A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: TIE-2 LIGANDS, METHODS OF MAKING AND USES THEREOF
; FILE REFERENCE: REG 330-F-PCT-US
; CURRENT APPLICATION NUMBER: US/10179,820
; CURRENT FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US/08/817,318
; PRIOR FILING DATE: 1999-09-16
; NUMBER OF SEQ ID NOS: 6
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; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2282
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Unknown Organism
; NAME/KEY: CDS
; LOCATION: (357)...(1847)
US-10-179-820-5
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Query Match 100.0%; Score 2282; DB 16; Length 2282;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GAATTCCTGGGTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGA 60
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Qy 301 TGGACGTGTGTTGGCCCTCAAGTTTGTCTAAGCTGTGGTTTATTAAGTGAAGAAAGT 360
Db 301 TGGACGTGTGTTGGCCCTCAAGTTTGTCTAAGCTGTGGTTTATTAAGTGAAGAAAGT 360
Qy 361 GGCAGATTGTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAAT 420
Db 361 GGCAGATTGTTTCTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAAT 420
Qy 421 TTCGGAAGAGCATGACAGCATAGGAAAGAACAAATATCAGGTCCAGCATGGGTCTGCA 480
Db 421 TTCGGAAGAGCATGACAGCATAGGAAAGAACAAATATCAGGTCCAGCATGGGTCTGCA 480
Qy 481 GGTACACTTTCCTCTCCAGAGATGGACAACTGCGCTCTTCCTCCAGCCCTTAGGT 540
Db 481 GGTACACTTTCCTCTCCAGAGATGGACAACTGCGCTCTTCCTCCAGCCCTTAGGT 540
Qy 541 CCAATGCTGTGCAGAGGACGCGCGCTCGAATACGATGACTCGGTGAGAGGCTGCAAG 600
Db 541 CCAATGCTGTGCAGAGGACGCGCGCTCGAATACGATGACTCGGTGAGAGGCTGCAAG 600
Qy 601 TGCTGGAGAACATCATGGAAGAACAACTCACTCACTGAGTGGCTTAATGAAGCTTGAGAAATTATATCC 660
Db 601 TGCTGGAGAACATCATGGAAGAACAACTCACTCACTGAGTGGCTTAATGAAGCTTGAGAAATTATATCC 660
Qy 661 AGGACAAATGAGAAAGAAATGTTAGATACAGCAGATGCAAGATGCAAGACCCAGAGCG 720
Db 661 AGGACAAATGAGAAAGAAATGTTAGATACAGCAGATGCAAGATGCAAGACCCAGAGCG 720
Qy 721 CTGTGATGATGAAATAGGACAAACCTTGTGAACCAACACAGCTGAGCAACCCGGAAGT 780
Db 721 CTGTGATGATGAAATAGGACAAACCTTGTGAACCAACACAGCTGAGCAACCCGGAAGT 780
Qy 781 TAACTGATGTGGAAGCCCAAGTATTAAATCAGACCAACAGACTTGAATTCAGCTCTTGG 840
Db 781 TAACTGATGTGGAAGCCCAAGTATTAAATCAGACCAACAGACTTGAATTCAGCTCTTGG 840
Qy 841 AACACTCCCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCCAGACCATGAAATAA 900
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Db 841 ||||| AACACTCCCTCTCGACAAACAAATTGGAAAAACAGATTTTGGACACAGACCAGTGAATAA 900
Qy 901 ACAAATTGCAAGATAGAACAGTTTCCCTAGAAAAGAGGTGCTAGCTATGGAAGACAAGC 960
Db 901 ACAAATTGCAAGATAGAACAGTTTCCCTAGAAAAGAGGTGCTAGCTATGGAAGACAAGC 960
Qy 961 ACATCATCAAACTACAGTCAATATAAAGAGAGAGAGATCAGCTACAGGTGTTAGTATCCA 1020
Db 961 ACATCATCCAACTACAGTCAATATAAAGAGAGAGAGATCAGCTACAGGTGTTAGTATCCA 1020
Qy 1021 AGCAAAATTCATCANTGAAAGAACTAGAAAAAATAATAGTACCTGCCACGGTGAAATAAT 1080
Db 1021 AGCAAAATTCATCANTGAAAGAACTAGAAAAAATAATAGTACCTGCCACGGTGAAATAAT 1080
Qy 1081 CAGTTCTTCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTACTCTCACTATGA 1140
Db 1081 CAGTTCTTCAAAAGCAGCAACATGATCTCATGAGACAGTTAATAACTTACTCTCACTATGA 1140
Qy 1141 TGTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAGAGAACAAATCAGCTTCA 1200
Db 1141 TGTCCACATCAAACTCAGCTAAGGACCCCACTGTTGCTAAGAGAACAAATCAGCTTCA 1200
Qy 1201 GAGACTGTGCTGAAGTATTCAAATCAGGACACACCAAAATGCGATCTACACGTTAACT 1260
Db 1201 GAGACTGTGCTGAAGTATTCAAATCAGGACACACCAAAATGCGATCTACACGTTAACT 1260
Qy 1261 TCCTTAATCTCAGAGAGATCAAGCCCTACTGTGATGGAAGCTGGAGGAGCGGGT 1320
Db 1261 TCCTTAATCTCAGAGAGATCAAGCCCTACTGTGATGGAAGCTGGAGGAGCGGGT 1320
Qy 1321 GGAACAATTATTCAGCGACGCTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAT 1380
Db 1321 GGAACAATTATTCAGCGACGCTGAGGATGGCAGCGTTGATTTTCAGAGGACTTGGAAAGAAT 1380
Qy 1381 ATAAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTTTCGC 1440
Db 1381 ATAAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTTTCGC 1440
Qy 1441 AACTGACTAATCAGACGCTGATGCTTAAATACACCTTAAAGACTGGGAGGGAATG 1500
Db 1441 AACTGACTAATCAGACGCTGATGCTTAAATACACCTTAAAGACTGGGAGGGAATG 1500
Qy 1501 AGCTTACTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATATAGGATTC 1560
Db 1501 AGCTTACTCATTTGATGAACATTTCTATCTCAAGTGAAGAACTCAATATAGGATTC 1560
Qy 1561 ACCTTAAAGGACTTACAGGACAGCCCGCAAAATAAGCAGCATCAGCCAAACCGAGAAATG 1620
Db 1561 ACCTTAAAGGACTTACAGGACAGCCCGCAAAATAAGCAGCATCAGCCAAACCGAGAAATG 1620
Qy 1621 ATTTAGCACAAAGGATGGAGACACCAAAATGATTTGCCAATGTTCAAAATGCTAA 1680
Db 1621 ATTTAGCACAAAGGATGGAGACACCAAAATGATTTGCCAATGTTCAAAATGCTAA 1680
Qy 1681 CAGGAGCTGTGTTGATGTCATGCTCTTCCAACTTGAACGGAATGTAATCTATCCAC 1740
Db 1681 CAGGAGCTGTGTTGATGTCATGCTCTTCCAACTTGAACGGAATGTAATCTATCCAC 1740
Qy 1741 AGAGGCAAGACACAAATAAGTTTCAACGGCATTAATGTTACTACTGGAAGGCTCAGGCT 1800
Db 1741 AGAGGCAAGACACAAATAAGTTTCAACGGCATTAATGTTACTACTGGAAGGCTCAGGCT 1800
Qy 1801 ATTGCTCAAGGCCACCAACCATGATGATCCGACAGAGATTTCTTAAACATCCAGTCCA 1860
Db 1801 ATTGCTCAAGGCCACCAACCATGATGATCCGACAGAGATTTCTTAAACATCCAGTCCA 1860
Qy 1861 CCTGAGGAATGCTCTCGAACTTATTTTCAAGACTTAAAGCCAGTGCACTGAAAGTCAAGG 1920
Db 1861 CCTGAGGAATGCTCTCGAACTTATTTTCAAGACTTAAAGCCAGTGCACTGAAAGTCAAGG 1920
Qy 1921 CTGCGCACTGTGCTCTCTTCCACACAGAGGCGGTGCTCGGTGCTGACGGGACCCACA 1980

Db 1921 CTGCGCACTGTGCTCTCTTCCACACAGAGGCGGTGCTCGGTGCTGACGGGACCCACA 1980
Qy 1981 TGCTCCAGATTAGAGCTGTAAACTTTTATCATCTTAAACTTTGCACTCACTTAAACGACCAA 2040
Db 1981 TGCTCCAGATTAGAGCTGTAAACTTTTATCATCTTAAACTTTGCACTCACTTAAACGACCAA 2040
Qy 2041 GCAAGCCCTTAAACATCCATTAATTTGATTTAGACAGAACACCTTATGCAAGATGAACCCG 2100
Db 2041 GCAAGCCCTTAAACATCCATTAATTTGATTTAGACAGAACACCTTATGCAAGATGAACCCG 2100
Qy 2101 AGCTCAGAAATCAGACTGACAGTTTACAGACGCTGTGTCAAAACCAAGAAATGTTATGTG 2160
Db 2101 AGCTCAGAAATCAGACTGACAGTTTACAGACGCTGTGTCAAAACCAAGAAATGTTATGTG 2160
Qy 2161 CAAAGTTTATCAGTAAATAAAGCTGAAACAGAACTTATGTTATACAAATCAGATCATCT 2220
Db 2161 CAAAGTTTATCAGTAAATAAAGCTGAAACAGAACTTATGTTATACAAATCAGATCATCT 2220
Qy 2221 TGGAACTGCACTTCTTCTGAGCACTGTTTATACACTGTGTAATACCATATGTCCTGAAT 2280
Db 2221 TGGAACTGCACTTCTTCTGAGCACTGTTTATACACTGTGTAATACCATATGTCCTGAAT 2280
Qy 2281 TC 2282
Db 2281 TC 2282

RESULT 7

US-10-603-293-5
; Sequence 5, Application US/10603293
; Publication No. US20050100906A1
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel et al.
; TITLE OF INVENTION: Tie-2 Ligands, Methods of Making and Uses Thereof
; FILE REFERENCE: REG 330-G-PCT-US
; CURRENT APPLICATION NUMBER: US/10/603,293
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: US/08/930,721
; PRIOR FILING DATE: FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US96/04806
; PRIOR FILING DATE: FILING DATE: 1996-04-05
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: PCT/US95/12935
; PRIOR FILING DATE: FILING DATE: 1995-10-06
; PRIOR APPLICATION NUMBER: APPLICATION NUMBER: 08/418,595
; PRIOR FILING DATE: FILING DATE: 1996-04-05
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 2282
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (357)..(1844)
US-10-603-293-5

Query Match 100.0%; Score 2282; DB 21; Length 2282;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2282; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAATTCCTGGGTTGGTGTGTTTATCTCTCCAGCCCTGAGGGGAGGAAACACCTGTAGGA 60
Db 1 GAATTCCTGGGTTGGTGTGTTTATCTCTCCAGCCCTGAGGGGAGGAAACACCTGTAGGA 60
Qy 61 TCTGGGAGAGAGAAACAAAGGACCGTGAAGCTGCTGTAAAAGCTGACACAGCCCTC 120
Db 61 TCTGGGAGAGAGAAACAAAGGACCGTGAAGCTGCTGTAAAAGCTGACACAGCCCTC 120
Qy 121 CCAAGTGAAGGAGGACTTCTTCTCCCACTGCAATCTGACAGTTTACTGCACTGCGAGAG 180
Db 121 CCAAGTGAAGGAGGACTTCTTCTCCCACTGCAATCTGACAGTTTACTGCACTGCGAGAG 180
Qy 181 AACACAGCAGTAAACACCGGTTGCTACTGGAAAAAGAGGAAAGAACTTTCATTG 240

[illegible]

1361	Db	TCCCTAATTTCTACAGAAAGAGATCAAGGCCCTACTGTGTGCATGGAAGCTGGAGGAGGCGGGT	1321
1321	Qy	GGACAAATTTATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGACATTTGAAAGAAT	1380
1321	Db		
1321	Qy	GGACAAATTTATTCAGCGACGTGAGGATGGCAGCGTTGATTTTTCAGAGACATTTGAAAGAAT	1380
1381	Qy	ATAAGTGGGATTTGGTAAACCTTTACGAGGAATATTTGGCTGGGAATATGATTTGTTTCGC	1440
1381	Db	ATAAGTGGGATTTGGTAAACCTTTACGAGGAATATTTGGCTGGGAATATGATTTGTTTCGC	1440
1441	Qy	AACGTGACTTAATCAGCAACGCTATGTGCTTAAATACACCTTTAAAGACTCGGAAGGGAATG	1500
1441	Db	AACGTGACTTAATCAGCAACGCTATGTGCTTAAATACACCTTTAAAGACTCGGAAGGGAATG	1500
1501	Qy	AGGCTTACTCAATTTGATGAACATTTCTCTCAAGTGAAGAACTCAATATAGGATTC	1560
1501	Db	AGGCTTACTCAATTTGATGAACATTTCTCTCAAGTGAAGAACTCAATATAGGATTC	1560
1561	Qy	ACCTTAAAGGACTTTACAGGACACGCGGCAAAATATAGCAGCATCAGCCACACGAGGAATG	1620
1561	Db	ACCTTAAAGGACTTTACAGGACACGCGGCAAAATATAGCAGCATCAGCCACACGAGGAATG	1620
1621	Qy	ATTTTACACAAAGGATGGAGACAAACGACAAATGTATTTGCCAATGTTCACAAATGCTAA	1680
1621	Db	ATTTTACACAAAGGATGGAGACAAACGACAAATGTATTTGCCAATGTTCACAAATGCTAA	1680
1681	Qy	CAGAGGCTCGTGGTTTGATGCAATGTGGTCTCTCCAACTTTGAAACGGAATGTACTATCCAC	1740
1681	Db	CAGAGGCTCGTGGTTTGATGCAATGTGGTCTCTCCAACTTTGAAACGGAATGTACTATCCAC	1740
1741	Qy	AGAGGCAGAAACAAATAAAGTTCCAAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCT	1800
1741	Db	AGAGGCAGAAACAAATAAAGTTCCAAACGGCATTTAAATGGTACTACTGGAAGGCTCAGGCT	1800
1801	Qy	ATTTCGTCAAAGGCCAACCAACCATGATCCGACGACAGATTTCTAAACATCCCACTCCA	1860
1801	Db	ATTTCGTCAAAGGCCAACCAACCATGATCCGACGACAGATTTCTAAACATCCCACTCCA	1860
1861	Qy	CCTCAGGAACGTGCTCGAACTATTTTCAAGACTTAAGCCCACTGACCTGAAAGTCACCG	1920
1861	Db	CCTCAGGAACGTGCTCGAACTATTTTCAAGACTTAAGCCCACTGACCTGAAAGTCACCG	1920
1921	Qy	CTCGCACTGTGCTCTTCCACACAGAGGGCGTGTGCTCGTGTGTCAGCGGACCCACA	1980
1921	Db	CTCGCACTGTGCTCTTCCACACAGAGGGCGTGTGCTCGTGTGTCAGCGGACCCACA	1980
1981	Qy	TGCTCCAGATTAGAGCCTGTAAACTTTATCACTTTAACTTGCACTACTTTAAACGGACCAA	2040
1981	Db	TGCTCCAGATTAGAGCCTGTAAACTTTATCACTTTAACTTGCACTACTTTAAACGGACCAA	2040
2041	Qy	GCAAGACCTTAAACATCCATAATTTGTGATTAGACAGAACACCTTATGCAAGATGAACCCG	2100
2041	Db	GCAAGACCTTAAACATCCATAATTTGTGATTAGACAGAACACCTTATGCAAGATGAACCCG	2100
2101	Qy	AGGCTGAGAAATCAGACTGACAGTTTACAGACGTGTGTGTACAAACGAGAAATGTTATGTG	2160
2101	Db	AGGCTGAGAAATCAGACTGACAGTTTACAGACGTGTGTGTACAAACGAGAAATGTTATGTG	2160
2161	Qy	CAGTTTATCAGTAATAATACCTGGAACAGAACACTTATGTGTTATACAAATACATCATCT	2220
2161	Db	CAGTTTATCAGTAATAATACCTGGAACAGAACACTTATGTGTTATACAAATACATCATCT	2220
2221	Qy	TGGAACCTGCATCTTCTTGAGCACTGTTTATACACTGTGTAAATACCATATGTCTCTGAAT	2280
2221	Db	TGGAACCTGCATCTTCTTGAGCACTGTTTATACACTGTGTAAATACCATATGTCTCTGAAT	2280
2281	Qy	TC 2282	
2281	Db	TC 2282	

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: Sequence 5, Application US/10928911
: Publication No. US20050106099A1
: GENERAL INFORMATION:
:
: APPLICANT: Davis, Samuel
: APPLICANT: Yancopoulos, George D.
: TITLE OF INVENTION: Expressed Ligand - Vari
: TITLE OF INVENTION: Intercellular Signal
: FILE REFERENCE: REG 333X
: CURRENT APPLICATION NUMBER: US/10/928,911
: CURRENT FILING DATE: 2004-08-27
: PRIOR APPLICATION NUMBER: 10/225,060
: PRIOR FILING DATE: 2002-08-21
: PRIOR APPLICATION NUMBER: 09/709,188
: PRIOR FILING DATE: 2000-11-09
: PRIOR APPLICATION NUMBER: 08/740,223
: PRIOR FILING DATE: 1996-10-25
: NUMBER OF SEQ ID NOS: 30
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 2282
: TYPE: DNA
: ORGANISM: Homo sapien
US-10-928-911-5

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Query Match	100.0%;	Score 2282;	DB 21;	Length 2282;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2282;	Conservative 0;	Mismatches 0;	Indels 0;	

Qy	1	GAATTCCTGGGTTGGTGTATTCTCCTCCAGCCTTGAGGAGGGAAACAACACTGTAGGA	60
Db	1	GAATTCCTGGGTTGGTGTATTCTCCTCCAGCCTTGAGGAGGGAAACAACACTGTAGGA	60
Qy	61	TCTGGGAGAGAGGAAACAAGGACCGTGAAGAGCTCTCTGTAAAGCTGACACAGCCCTC	120
Db	61	TCTGGGAGAGAGGAAACAAGGACCGTGAAGAGCTCTCTGTAAAGCTGACACAGCCCTC	120
Qy	121	CCAAGTGAGCAGGACTGTTCTTCCACTGCAATCTGACAGTTTACTGCAATGCCCTGGAG	180
Db	121	CCAAGTGAGCAGGACTGTTCTTCCACTGCAATCTGACAGTTTACTGCAATGCCCTGGAG	180
Qy	181	AACACAGCAGTAAAAACACAGGTTTGTCTACTGAAAAAGAGAAAGAGACTTTCATTG	240
Db	181	AACACAGCAGTAAAAACACAGGTTTGTCTACTGAAAAAGAGAAAGAGACTTTCATTG	240
Qy	241	ACGACCCAGCCATGCGACGCTAGCAGCCCTGCTTTCAGACGGCAGCAGCTCGGGACTC	300
Db	241	ACGACCCAGCCATGCGACGCTAGCAGCCCTGCTTTCAGACGGCAGCAGCTCGGGACTC	300
Qy	301	TGGACGTGTGTTGGCTTCAAGTTTGTAAAGCTGCTGTTTATTACTGAAGAAAGAAATGT	360
Db	301	TGGACGTGTGTTGGCTTCAAGTTTGTAAAGCTGCTGTTTATTACTGAAGAAAGAAATGT	360
Qy	361	GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAAT	420
Db	361	GGCAGATTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCCGAGCCTATAACAAT	420
Qy	421	TTCGAAGAGCATGACACAGCATAGAAAGAACCAATATCAGTCCAGCATGGTCTCTGCA	480
Db	421	TTCGAAGAGCATGACACAGCATAGAAAGAACCAATATCAGTCCAGCATGGTCTCTGCA	480
Qy	481	GCTACACTTTCCTCTGCGCAGAGTGGCAAACTGCGGCTCTTCTCCAGCCCTCAGTGT	540
Db	481	GCTACACTTTCCTCTGCGCAGAGTGGCAAACTGCGGCTCTTCTCCAGCCCTCAGTGT	540
Qy	541	CCAATGCTGTGAGAGGGACGCGCGCTCGAATAAATGCTCGGTGAGAGGCTGCAAG	600
Db	541	CCAATGCTGTGAGAGGGACGCGCGCTCGAATAAATGCTCGGTGAGAGGCTGCAAG	600
Qy	601	TGCTGGAGAACATCATGGAAGAACACACTCAGTGGCTAATGAAGCTTGAGAATTATATCC	660
Db	601	TGCTGGAGAACATCATGGAAGAACACACTCAGTGGCTAATGAAGCTTGAGAATTATATCC	660
Qy	661	AGGACAACATGAAGAAAGAAATGGTAGAGATACAGCAGAAATCAGTACAGAACCCAGACGG	720

[illegible]

1201 TGCTGAAGTATTCAAAATCAGGACACACCAATGGCATCTACAGTTAACTCCCTAA 1260
1268 TTCTCAGAGAGATCAAGSCCTACTGTGATGGAAGCTGGAGGAGGGGTGGCAAT 1327
1261 TTCTCAGAGAGATCAAGSCCTACTGTGATGGAAGCTGGAGGAGGGGTGGCAAT 1320
1328 TATTACGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGAAGAATATAAGT 1387
1321 TATTACGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGAAGAATATAAGT 1380
1388 GGAATTTGGTAACCTTCAGGAGAAATATGGCTGGGAATGAGTTTTCGCACTGAC 1447
1381 GGAATTTGGTAACCTTCAGGAGAAATATGGCTGGGAATGAGTTTTCGCACTGAC 1440
1448 TAATCAGCAACGCTATGTGCTTAAATATACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1507
1441 TAATCAGCAACGCTATGTGCTTAAATATACACCTTAAAGACTGGGAAGGAAATGAGGCTTA 1500
1508 CTCATTGTATGAACATTTCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567
1501 CTCATTGTATGAACATTTCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560
1568 AGGACTTACAGGACAGCGCGGAAAATTAAGCAGCATCAGCAACCCAGGAAATGATTTAG 1627
1561 AGGACTTACAGGACAGCGCGGAAAATTAAGCAGCATCAGCAACCCAGGAAATGATTTAG 1620
1628 CACAAAGGATGGAGACCAACCAATATTTTCAATGTTCAAAATGCTTAACAGGAG 1687
1621 CACAAAGGATGGAGACCAACCAATATTTTCAATGTTCAAAATGCTTAACAGGAG 1680
1688 CTGGTGGTTTGTGATGCTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGGCA 1747
1681 CTGGTGGTTTGTGATGCTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGGCA 1740
1748 GAACACAAATAGTTTCAACGGCAATTAATGGTACTACTGAAAGGCTCAGGCTATTCGCT 1807
1741 GAACACAAATAGTTTCAACGGCAATTAATGGTACTACTGAAAGGCTCAGGCTATTCGCT 1800
1808 CAAGGCCACAAACCATGATGATCGGACAGCAGATTTCTAAACATCCAGTCCACCTGAG 1867
1801 CAAGGCCACAAACCATGATGATCGGACAGCAGATTTCTAAACATCCAGTCCACCTGAG 1860
1868 AACTGTCTGAACTTATTTTCAAGACTTAAAGCCAGTGCCTGAAAGTCAAGGCTGCGCA 1927
1861 AACTGTCTGAACTTATTTTCAAGACTTAAAGCCAGTGCCTGAAAGTCAAGGCTGCGCA 1920
1928 CTGTGCTCTTCCACACAGAGGGCGTGTGCTGGTGTGAGCGGACCCACATGCTCCA 1987
1921 CTGTGCTCTTCCACACAGAGGGCGTGTGCTGGTGTGAGCGGACCCACATGCTCCA 1980
1988 GATTAGAGCTGTAACTTTATCACTTAACTTGCATCACTTAACGACCAACAGCAAGAC 2047
1981 GATTAGAGCTGTAACTTTATCACTTAACTTGCATCACTTAACGACCAACAGCAAGAC 2040
2048 CCTAAACATCCATAATTTGATTAGACAGAACACTATGCAAGATCAACCCAGGCTGA 2107
2041 CCTAAACATCCATAATTTGATTAGACAGAACACTATGCAAGATCAACCCAGGCTGA 2100
2108 GAATCAGACTGACAGTTTACAGAGCTGTGCTCAACCAAGAAATGTTATGTGCAAGTTT 2167
2101 GAATCAGACTGACAGTTTACAGAGCTGTGCTCAACCAAGAAATGTTATGTGCAAGTTT 2160
2168 ATCAGTAAATACTGGGAAAACAGAAACACTTATGTTTATCAATACAGATCATCTTGGAACT 2227
2161 ATCAGTAAATACTGGGAAAACAGAAACACTTATGTTTATCAATACAGATCATCTTGGAACT 2220
2228 GCATTTCTTGAGCAGCTGTTTATACACTGTGTAATACCCATATGCTCT 2276
2221 GCATTTCTTGAGCAGCTGTTTATACACTGTGTAATATACCCATATGCTCT 2269

US-09-998-833-3
; Sequence 3, Application US/0998833
; Publication No. US20030082187A1
; GENERAL INFORMATION:
; APPLICANT: THORPE, PHILIP E.
; APPLICANT: RAN, SOPHIA
; TITLE OF INVENTION: CANCER TREATMENT METHODS USING ANTIBODIES TO
; TITLE OF INVENTION: AMINOPHOSPHOLIPIDS
; FILE REFERENCE: 4001.002200
; CURRENT APPLICATION NUMBER: US/09/998,833
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: US/09/351,543
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-998-833-3

Query Match 99.4%; Score 2269; DB 10; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGTGTTTATCTCTCCAGCCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 67
DB 1 TGGGTTGGTGTGTTTATCTCTCTCCAGCCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 60
QY 68 AGAGAGCAACNAAGGACCGTGAAGCTGCTCTGTAAGCTGACACAGCCCTCCCAAGTG 127
DB 61 AGAGAGCAACNAAGGACCGTGAAGCTGCTCTGTAAGCTGACACAGCCCTCCCAAGTG 120
QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGCTTTACTGCATGCCCTGGAGAGAACACAG 187
DB 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGCTTTACTGCATGCCCTGGAGAGAACACAG 180
QY 188 CAGTAAAAACCAAGTTTGTCTTGGAAAAAGAGAGAAAGAGAACTTTTCATTGACGAGCC 247
DB 181 CAGTAAAAACCAAGTTTGTCTTGGAAAAAGAGAGAAAGAGAACTTTTCATTGACGAGCC 240
QY 248 CAGCCATGGCAGGCTAGCAGCCCTGGTTTTCAGACGCGCAGCAGCTCGGAGCTCTGGAGCT 307
DB 241 CAGCCATGGCAGGCTAGCAGCCCTGGTTTTCAGACGCGCAGCAGCTCGGAGCTCTGGAGCT 300
QY 308 GTGTTTGGCCCTCAAGTTTGTCTGTAAGCTGCTGTTTATTTACTGAAAGAAAGAAATGTGGCAGAT 367
DB 301 GTGTTTGGCCCTCAAGTTTGTCTGTAAGCTGCTGTTTATTTACTGAAAGAAAGAAATGTGGCAGAT 360
QY 368 TGTGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCCGCGAGCCCTATTAACAACTTTTCGGAA 427
DB 361 TGTGTTTCTTTTACTCTGAGCTGTGATCTTGTCTTGGCCGCGAGCCCTATTAACAACTTTTCGGAA 420
QY 428 GAGCATGACAGCATAGGAAGAAGCAATATCAGGTCAGCATGGGTCCTGCGAGCTACAC 487
DB 421 GAGCATGACAGCATAGGAAGAAGCAATATCAGGTCAGCATGGGTCCTGCGAGCTACAC 480
QY 488 TTTTCTCTCCGAGAGATGCAACAACTGCGCTCTTCTCCAGCCCTCAGTGTCCAATGTC 547
DB 481 TTTTCTCTCCGAGAGATGCAACAACTGCGCTCTTCTCCAGCCCTCAGTGTCCAATGTC 540
QY 548 TGTGCGAGAGGAGCGCGCTCGAATAACGATGATCTCGGTGCGAGAGGCTGCAAGTGTCTGGA 607
DB 541 TGTGCGAGAGGAGCGCGCTCGAATAACGATGATCTCGGTGCGAGAGGCTGCAAGTGTCTGGA 600
QY 608 GAACATCATGGAAGAAACAACACTCAGTGGCTTAATGAAGCTTGAAGTTATATCCAGGACAA 667
DB 601 GAACATCATGGAAGAAACAACACTCAGTGGCTTAATGAAGCTTGAAGTTATATCCAGGACAA 660
QY 668 CATGGAAGAAAGAAATGCTAGAGATACAGAGAAATGCAAGTACAGACCGGCTGTGAT 727
DB 661 CATGGAAGAAAGAAATGCTAGAGATACAGAGAAATGCAAGTACAGACCGGCTGTGAT 720

Qy	728	GATAGAAATAGGGACAAACCTGTTGAAACAAACAGCTGAGCAAAACGCGGAAGTTAACTGA	787
Db	721	GATAGAAATAGGGACAAACCTGTTGAAACAAACAGCTGAGCAAAACGCGGAAGTTAACTGA	780
Qy	788	TGTCGAAGCCCAAGCTATTAAATCAGACCCAGAGACTTTGAACTTCAGCTCTTTGGAACAACCTC	847
Db	781	TGTCGAAGCCCAAGCTATTAAATCAGACCCAGAGACTTTGAACTTCAGCTCTTTGGAACAACCTC	840
Qy	848	CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCGACACCAAGTGAATAAACAAATTT	907
Db	841	CCTCTCGACAAACAAATTTGGAAAAACAGATTTTGGACCGACACCAAGTGAATAAACAAATTT	900
Qy	908	GCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGCTAGCTATGGAAGACAAAGCACATCAT	967
Db	901	GCAAGATAAGAACAGTTTCTTAGAAAAAGAGGTGCTAGCTATGGAAGACAAAGCACATCAT	960
Qy	968	CCAACTACAGTCAATAAAGGAAGAGAAGATCAGCTACAGTGTGTAGTATCCCAAGCAAAA	1027
Db	961	CCAACTACAGTCAATAAAGGAAGAGAAGATCAGCTACAGTGTGTAGTATCCCAAGCAAAA	1020
Qy	1028	TTCCATCATTTGAAGAACTAGAAAAAAAATAGTGACTTGCCACGGTGAAATAATTCAGTTCT	1087
Db	1021	TTCCATCATTTGAAGAACTAGAAAAAAAATAGTGACTTGCCACGGTGAAATAATTCAGTTCT	1080
Qy	1088	TCAAAAGCAGCAACATGATCTCATGAGAGACAGTTTAATACTGACTATGATGTCAC	1147
Db	1081	TCAAAAGCAGCAACATGATCTCATGAGAGACAGTTTAATACTGACTATGATGTCAC	1140
Qy	1148	ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAGAACAATACTAGCTTCAGAGACTG	1207
Db	1141	ATCAAACTCAGCTAAGGACCCCACTGTTGCTAAAGAGAACAATACTAGCTTCAGAGACTG	1200
Qy	1208	TGCTGAAGTATTTCAAACTCAGGACACACCAAAATGGCATCTACACGTTTAACTTCCCTAA	1267
Db	1201	TGCTGAAGTATTTCAAACTCAGGACACACCAAAATGGCATCTACACGTTTAACTTCCCTAA	1260
Qy	1268	TTCTACAGAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGGCGCGGTGGACAAT	1327
Db	1261	TTCTACAGAAGAGATCAAGGCCTACTGTGACATGGAAGCTGGAGGCGCGGTGGACAAT	1320
Qy	1328	TATTCAGGCGCTGAGGATGCGCAGGTTGATTTTCAGAGGACTTTGGAAGAANTATAAAGT	1387
Db	1321	TATTCAGGCGCTGAGGATGCGCAGGTTGATTTTCAGAGGACTTTGGAAGAANTATAAAGT	1380
Qy	1388	GGGATTTTGGTAAACCTTTCAGGAGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC	1447
Db	1381	GGGATTTTGGTAAACCTTTCAGGAGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC	1440
Qy	1448	TAATCAGCAACGCTATGTGCTTAAAAATACACCTTTAAAGACTGGGAAGGAATGAGGCTTA	1507
Db	1441	TAATCAGCAACGCTATGTGCTTAAAAATACACCTTTAAAGACTGGGAAGGAATGAGGCTTA	1500
Qy	1508	CTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTTCACTTAA	1567
Db	1501	CTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTTCACTTAA	1560
Qy	1568	AGGACTTACGGGACAGCCGCAAAATAAGCAGCATCAGCCAACCGAGGAATGATTTTAG	1627
Db	1561	AGGACTTACGGGACAGCCGCAAAATAAGCAGCATCAGCCAACCGAGGAATGATTTTAG	1620
Qy	1628	CACAAAGGATGGAGACACGACAAATGTATTTGCAAAATGTTTCACAAATGCTTAAACAGGAGG	1687
Db	1621	CACAAAGGATGGAGACACGACAAATGTATTTGCAAAATGTTTCACAAATGCTTAAACAGGAGG	1680
Qy	1688	CTGTTGTTTGAATGATGTGTTCTTCCAACTTGAAACGGAATGTACTATCCACAGAGGCA	1747
Db	1681	CTGTTGTTTGAATGATGTGTTCTTCCAACTTGAAACGGAATGTACTATCCACAGAGGCA	1740
Qy	1748	GAAACAAATTAAGTTTCAACGCAATTAATAGTACTTCTGGAAGAGGCTCAGGCTATTGCT	1807
Db	1741	GAAACAAATTAAGTTTCAACGCAATTAATAGTACTTCTGGAAGAGGCTCAGGCTATTGCT	1800
Qy	1808	CAAGGCCACAAACCATGATGATCCGACACAGCAGATTTTCTTAAACATCCCAAGTCCACCTGAGG	1867

Db	1801	CAAGGCCACAAACATGATGATCGACAGCAGAGATTTCTAAACATCCAGATCCACCTGAGG	1860
Qy	1868	AACGTGCTCGAACTATTTTCAAGAGACTTAAGCCAGTGCACCTGAAAAGTCAACGGCTGCGCA	1927
Db	1861	AACGTGCTCGAACTATTTTCAAGAGACTTAAGCCAGTGCACCTGAAAAGTCAACGGCTGCGCA	1920
Qy	1928	CTGTGTCTCTTCCACACACAGAGGGCGTGTGCTCGTGTGACGGGACCCACATGCTCCA	1987
Db	1921	CTGTGTCTCTTCCACACAGAGGGCGTGTGCTCGTGTGACGGGACCCACATGCTCCA	1980
Qy	1988	GATTAGAGCCTGTAAACTTTATCAGCTTAAACTTTGCATCAGCTTAACGGACCAAGCAAGAC	2047
Db	1981	GATTAGAGCCTGTAAACTTTATCAGCTTAAACTTTGCATCAGCTTAACGGACCAAGCAAGAC	2040
Qy	2048	CCTAAACATCCATAATTGTGATTAGACAGAAACACCTATGCAAGAGATGAAACCCGAGGCTGA	2107
Db	2041	CCTAAACATCCATAATTGTGATTAGACAGAAACACCTATGCAAGAGATGAAACCCGAGGCTGA	2100
Qy	2108	GAATCAGACTGACAGTTTATACAGACGCTGCTGTGCACAAACCAAGAATGTTATGTGCAAGTTT	2167
Db	2101	GAATCAGACTGACAGTTTATACAGACGCTGCTGTGCACAAACCAAGAATGTTATGTGCAAGTTT	2160
Qy	2168	ATCAGTAAATAACTGGAAAAACAGAAACACTTATGTTATACAATACAGATCATCTTGGAACT	2227
Db	2161	ATCAGTAAATAACTGGAAAAACAGAAACACTTATGTTATACAATACAGATCATCTTGGAACT	2220
Qy	2228	GCATCTTCTGAGCAGCTGTTTATACACTGTGTAAATACCATATGTCCT	2276
Db	2221	GCATCTTCTGAGCAGCTGTTTATACACTGTGTAAATACCATATGTCCT	2269

RESULT 11

US-10-101-510-460

; Sequence 460, Application US/10101510

; Publication No. US20030148295A1

; GENERAL INFORMATION:

; APPLICANT: WAN JACKSON

; APPLICANT: WANG, YIXIN

; TITLE OF INVENTION: EXPRESSION PROFILES AND METHODS OF USE

; FILE REFERENCE: 15117.0012

; CURRENT APPLICATION NUMBER: US/10/101.510

; CURRENT FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: 60/276,947

; PRIOR FILING DATE: 2001-03-20

; NUMBER OF SEQ ID NOS: 805

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 460

; LENGTH: 2269

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-101-510-460

Query March	99.4%	Score 2269;	DB 15;	Length 2269;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2269;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	8	TGGGTTGGTGTATTCTCTCCACAGCCCTTCAGGGAGGGAACAACACTGTAGGATCTCGGG	67	
Db	1	TGGGTTGGTGTATTCTCTCCACAGCCCTTCAGGGAGGGAACAACACTGTAGGATCTCGGG	60	
Qy	68	AGAGAGAAACAAGGACCGTGAAGCTGTCTGTAAAAGCTGCACACAGCCCTCCCAAGTG	127	
Db	61	AGAGAGAAACAAGGACCGTGAAGCTGTCTGTAAAAGCTGCACACAGCCCTCCCAAGTG	120	
Qy	128	AGCAGGACTGTGTTCTTCCCACTGCAACTCTGCACAGTTTACTGCATCGCTGGAGAGAAACACAG	187	
Db	121	AGCAGGACTGTGTTCTTCCCACTGCAACTCTGCACAGTTTACTGCATCGCTGGAGAGAAACACAG	180	
Qy	188	CAGTAAAAACAGGTTTGCTACTCGAAAAAGAGAGAAAGACTTTCATTGACGGACC	247	
Db	181	CAGTAAAAACAGGTTTGCTACTCGAAAAAGAGAGAAAGACTTTCATTGACGGACC	240	

QY 248 CAGCCATGGCAGCGTATGACGCTCTGGCTTTTCAACGCGCAGCAGCTCGGAGCTCTGACGCT 307
Db 241 CAGCCATGGCAGCGTATGACGCTCTGGCTTTTCAACGCGCAGCAGCTCGGAGCTCTGACGCT 300
QY 308 GTGTTTCCCTCAAGTTTGTAGCTGCTGCTTTTATTTACTGAGAGAAAGATGTGGCAGAT 367
Db 301 GTGTTTCCCTCAAGTTTGTAGCTGCTGCTTTTATTTACTGAGAGAAAGATGTGGCAGAT 360
QY 368 TGTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGCGCAGCCTATAACAACCTTTCCGAA 427
Db 361 TGTGTTTCTTTACTCTGAGCTGTGATCTTGTCTTGGCGCGCAGCCTATAACAACCTTTCCGAA 420
QY 428 GAGCATGGACAGCATAGGAAGAAAGCAATATCAGGTCAGCATGGGTCTGCGAGCTACAC 487
Db 421 GAGCATGGACAGCATAGGAAGAAAGCAATATCAGGTCAGCATGGGTCTGCGAGCTACAC 480
QY 488 TTTCTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTACGTTGCCAATGC 547
Db 481 TTTCTCTCTCCAGAGATGACAACTGCGCTCTTCTCCAGCCCTACGTTGCCAATGC 540
QY 548 TGTGCGAGGAGCGCGCGCTCGAATAACGATGACTCGGTGCAGAGGCTGCAAGTGTGGA 607
Db 541 TGTGCGAGGAGCGCGCGCTCGAATAACGATGACTCGGTGCAGAGGCTGCAAGTGTGGA 600
QY 608 GAAATCATGGAAGAAACAACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGGACAA 667
Db 601 GAACATCATGGAAGAAACAACTCAGTGGCTTAATGAAGCTTGAGAAATATATCCAGGACAA 660
QY 668 CATGAAGAAAGAAATGTTAGATACAGAGAAATGCGATGACTCGGTGCAGAGGCTGCAAGTGTGAT 727
Db 661 CATGAAGAAAGAAATGTTAGATACAGAGAAATGCGATGACTCGGTGCAGAGGCTGCAAGTGTGAT 720
QY 728 GATGAATATAGGACAACTGTTGAACCAACAGCTGAGCAACGCGGAGGTTAACTGA 787
Db 721 GATGAATATAGGACAACTGTTGAACCAACAGCTGAGCAACGCGGAGGTTAACTGA 780
QY 788 TGTGGAAGCCCAAGTATTAATCAGACACGAGACTTTGAACTTCAGCTCTTTGGAACACTC 847
Db 781 TGTGGAAGCCCAAGTATTAATCAGACACGAGACTTTGAACTTCAGCTCTTTGGAACACTC 840
QY 848 CTTCTCGACAAAACAAATTTGMAAAACAGATTTTGGACACGACGATGAAATTAACAATTT 907
Db 841 CTTCTCGACAAAACAAATTTGMAAAACAGATTTTGGACACGACGATGAAATTAACAATTT 900
QY 908 GCAGATATAGACAGTTTCTTAGAAAAGAGGCTAGCTATGAAAGCAAGCAACATCAT 967
Db 901 GCAAGATATAGACAGTTTCTTAGAAAAGAGGCTAGCTATGAAAGCAAGCAACATCAT 960
QY 968 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAA 1027
Db 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAAA 1020
QY 1028 TTCCATCATTGAAGAACTAGAAAAAATAAGTGACTGCGCAGGTGAATATTCAGTTCT 1087
Db 1021 TTCCATCATTGAAGAACTAGAAAAAATAAGTGACTGCGCAGGTGAATATTCAGTTCT 1080
QY 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAAATTAACCTTACTGATATGATGCTCAC 1147
Db 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAAATTAACCTTACTGATATGATGCTCAC 1140
QY 1148 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAAACAAATCAGCTTCAGAGACTG 1207
Db 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAGAAACAAATCAGCTTCAGAGACTG 1200
QY 1208 TGCTGAAGTATTAATCAGGACACACCAAAATGGCAATCTACAGTTTAAATTCCTTAA 1267
Db 1201 TGCTGAAGTATTAATCAGGACACACCAAAATGGCAATCTACAGTTTAAATTCCTTAA 1260
QY 1268 TTCTACAGAGATCAAGGCTTACTGTGACATGGAAGCTGAGGAGCGGCTGGACAAAT 1327
Db 1261 TTCTACAGAGATCAAGGCTTACTGTGACATGGAAGCTGAGGAGCGGCTGGACAAAT 1320
QY 1328 TATTACGCGCTGAGGATGCGAGGTTGATTTTTCAGAGGACTTGGAAAGAAATATAAGT 1387

Db 1321 TATTACGCGCTGAGGATGGCAGCTTGTGATTTTTCAGAGGACTTGGAAAGAAATATAAGT 1380
QY 1388 GGGATTTGGTAAACCCCTTCAGGAGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1447
Db 1381 GGGATTTGGTAAACCCCTTCAGGAGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1440
QY 1448 TAAATCAGCAACCGTATGTGCTTTAAATACACCTTAAAGACTGGGAAAGGAAATGAGGCTTA 1507
Db 1441 TAAATCAGCAACCGTATGTGCTTTAAATACACCTTAAAGACTGGGAAAGGAAATGAGGCTTA 1500
QY 1508 CTCATTGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATATTAGGATTCACCTTAA 1567
Db 1501 CTCATTGTATGAACATTTCTCTCTCAAGTGAAGAACTCAATATTAGGATTCACCTTAA 1560
QY 1568 AGGACTTTCAGGAGACGCGGCAAAATAAGCAGCATCAGCAACCCAGGAAATGATTTAG 1627
Db 1561 AGGACTTTCAGGAGACGCGGCAAAATAAGCAGCATCAGCAACCCAGGAAATGATTTAG 1620
QY 1628 CACAAAGGATGGAGACAAACGACAAATGATTTGCAAAATGTTCAAAATGCTTAACAGGAG 1687
Db 1621 CACAAAGGATGGAGACAAACGACAAATGATTTGCAAAATGTTCAAAATGCTTAACAGGAG 1680
QY 1688 CTGCTGTTTGTATGATGTGCTCTTCCAACTTGAACGGAATGCTATCTATCCACAGAGCA 1747
Db 1681 CTGCTGTTTGTATGATGTGCTCTTCCAACTTGAACGGAATGCTATCTATCCACAGAGCA 1740
QY 1748 GAAACAAATAAAGTTTCAACGGCAATTAATGTTACTACTGGAAGGCTCAGGCTATTCGCT 1807
Db 1741 GAAACAAATAAAGTTTCAACGGCAATTAATGTTACTACTGGAAGGCTCAGGCTATTCGCT 1800
QY 1808 CAAGGCCCAACCATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG 1867
Db 1801 CAAGGCCCAACCATGATGATCCGACAGCAGATTTCTAAACATCCAGTCCACCTGAGG 1860
QY 1868 AACTGCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACTGAAAGTCAACGCTGCGCA 1927
Db 1861 AACTGCTCGAACTATTTTCAAAGACTTAAAGCCAGTGCACTGAAAGTCAACGCTGCGCA 1920
QY 1928 CTGCTGCTCTTCCACACAGAGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987
Db 1921 CTGCTGCTCTTCCACACAGAGGCGTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980
QY 1988 GATTAGAGCTGTAAACTTTTATCACTTAAACTTTGATCACTTAAACGACCAAGCAAGAC 2047
Db 1981 GATTAGAGCTGTAAACTTTTATCACTTAAACTTTGATCACTTAAACGACCAAGCAAGAC 2040
QY 2048 CCTAAACATCCATAATTTGATTTAGACAGAACACCTATGCAAAAGATGAACCCGAGGCTGA 2107
Db 2041 CCTAAACATCCATAATTTGATTTAGACAGAACACCTATGCAAAAGATGAACCCGAGGCTGA 2100
QY 2108 GAATCAGACTGACAGTTTACAGAGCGTGTGCTGCTCAACACCAAGAAATGTTATGTGCAAGTTT 2167
Db 2101 GAATCAGACTGACAGTTTACAGAGCGTGTGCTGCTCAACACCAAGAAATGTTATGTGCAAGTTT 2160
QY 2168 ATCAGTAAATACTGGAAAAACAGAAACCTTATGTTTATACAAATCAGATCATCTTGGAACT 2227
Db 2161 ATCAGTAAATACTGGAAAAACAGAAACCTTATGTTTATACAAATCAGATCATCTTGGAACT 2220
QY 2228 GCATTCTTCTGAGCACTGTTTATACACTGTGTAATATCCCATATGCTCT 2276
Db 2221 GCATTCTTCTGAGCACTGTTTATACACTGTGTAATATCCCATATGCTCT 2269

RESULT 12
US-10-373-561-3
; Sequence 3, Application US/10373561
; Publication No. US20030175276A1
; GENERAL INFORMATION:
; APPLICANT: Philip E. Thorpe
; APPLICANT: Rolf A. Brekken
; TITLE OF INVENTION: ANTIBODY METHODS FOR SELECTIVELY INHIBITING VEGF
; FILE REFERENCE: 4001.002582

;
; CURRENT APPLICATION NUMBER: US/10/373,561
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US/09/561,499
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/131,432
; PRIOR FILING DATE: 1999-04-28
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-373-561-3

Query Match 99.4%; Score 2269; DB 16; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 TGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 67
DB 1 TGGGTTGGTGTATCTCTCCAGCCTTGAGGGAGGGAACAACACTGTAGGATCTGGGG 60

QY 68 AGAGAGAAACAAAGACCTGAAAGCTCTGTGTAAGCTGACACAGCCCTCCCAAGTG 127
DB 61 AGAGAGAAACAAAGAGCCGTGAAAGCTCTGTGTAAGCTGACACAGCCCTCCCAAGTG 120

QY 128 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTGCGAGAGAAACACAG 187
DB 121 AGCAGGACTGTTCTTCCCACTGCAATCTGACAGTTTACTGTCATGCTGCGAGAGAAACACAG 180

QY 188 CAGTAAAAACCAAGTTTGTCTCTGGAAGAGGAAAGAGAGACTTTCATTTGACGGACC 247
DB 181 CAGTAAAAACCAAGTTTGTCTCTGGAAGAGGAAAGAGAGACTTTCATTTGACGGACC 240

QY 248 CAGCCATGCGAGGTAGAGCCCTGCTGTTTCAGACGGCAGAGCTCGGACCTCTGGAAGT 307
DB 241 CAGCCATGCGAGGTAGAGCCCTGCTGTTTCAGACGGCAGAGCTCGGACCTCTGGAAGT 300

QY 308 GTGTTTGCCCTCAAGTTTCTAAGCTGCTGGTTTATTACTGAAGAAAGAAATGTCGAGAT 367
DB 301 GTGTTTGCCCTCAAGTTTCTAAGCTGCTGGTTTATTACTGAAGAAAGAAATGTCGAGAT 360

QY 368 TGTGTTCTTTA CTGAGCTGTGATCTTCTGTGCGCGCAGCCTATPACAACTTTTCGGAA 427
DB 361 TGTGTTCTTTA CTGAGCTGTGATCTTCTGTGCGCGCAGCCTATPACAACTTTTCGGAA 420

QY 428 GAGCATGGAACATAGGAAGAAAGCAATATCAGGTCAGCATGGTCTGCGAGCTACAC 487
DB 421 GAGCATGGAACATAGGAAGAAAGCAATATCAGGTCAGCATGGTCTGCGAGCTACAC 480

QY 488 TTTCTCTCTGCGAGATGGAACACTGCGCTCTTCTCCAGCCCTACGTGTCOAATGC 547
DB 481 TTTCTCTCTGCGAGATGGAACACTGCGCTCTTCTCCAGCCCTACGTGTCOAATGC 540

QY 548 TGTGAGAGGACGGCCGCTCGAATACGATGACTCGGTGCGAGAGCTGCAAGTGTGGA 607
DB 541 TGTGAGAGGACGGCCGCTCGAATACGATGACTCGGTGCGAGAGCTGCAAGTGTGGA 600

QY 608 GAACATCATGGAACAAACACTCAGTGGCTATGAGCTTGAGATTATATCCAGACAA 667
DB 601 GAACATCATGGAACAAACACTCAGTGGCTATGAGCTTGAGATTATATCCAGACAA 660

QY 668 CATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAATGCAAGAACAGAGCTGTGAT 727
DB 661 CATGAAGAAAGAAATGGTAGAGATACAGCAGAAATGCAATGCAAGAACAGAGCTGTGAT 720

QY 728 GATAGAAATAGGACAAACCTGTTGAA CCAACAGCTGAGGAAACCGCGAAGTTAACTGA 787
DB 721 GATAGAAATAGGACAAACCTGTTGAA CCAACAGCTGAGGAAACCGCGAAGTTAACTGA 780

QY 788 TGTGGAAGCCCAAGTATTAAATCAGACACAGAGCTTGAATTCAGCTCTTGGAAACCTC 847
DB 781 TGTGGAAGCCCAAGTATTAAATCAGACACAGAGCTTGAATTCAGCTCTTGGAAACCTC 840

QY 848 CCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACCAGACCGAGTGAATAAACAATTT 907
DB 841 CCTCTCGACAAACAAATTTGAAAAACAGATTTTGGACCAGACCGAGTGAATAAACAATTT 900

QY 908 GCAAGATAAGAACAGTTTCTCTAGAAAAAGAGGTGTAGCTATGGAAGACAAACATCAT 967
DB 901 GCAAGATAAGAACAGTTTCTCTAGAAAAAGAGGTGTAGCTATGGAAGACAAACATCAT 960

QY 968 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAA 1027
DB 961 CCAACTACAGTCAATAAAGAGAGAAAGATCAGCTACAGGTGTTAGTATCCAAAGCAAA 1020

QY 1028 TTCCATCATTTGAAGAACTAGAAAAAATAAGTGTGCTCCAGCGTGAATAAATTCAGTTCT 1087
DB 1021 TTCCATCATTTGAAGAACTAGAAAAAATAAGTGTGCTCCAGCGTGAATAAATTCAGTTCT 1080

QY 1088 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAATAACTTACTGACTATGATGTCAC 1147
DB 1081 TCAAAAGCAGCAACATGATCTCATGGAGACAGTTTAATAACTTACTGACTATGATGTCAC 1140

QY 1148 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAAACAAATCAGCTTCAGAGACTG 1207
DB 1141 ATCAAACTCAGCTAAGGACCCCACTGTTGCTTAAAGAAACAAATCAGCTTCAGAGACTG 1200

QY 1208 TGCTGAAGTATTTCAAAATCAGGACACACCAAAATGGCATCTACACGTTTAAACATTCCTTAA 1267
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QY 1268 TTCTACAGAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGAGGCGGTGACAAAT 1327
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QY 1388 GGGATTTGGTAAACCTCTCAGGAGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1447
DB 1381 GGGATTTGGTAAACCTCTCAGGAGAAATATTTGGCTGGGAAATGAGTTTGTTCGCAACTGAC 1440

QY 1448 TAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTA 1507
DB 1441 TAATCAGCAACGCTATGTGCTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTA 1500

QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA 1567
DB 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGGATTCACCTTAA 1560

QY 1568 AGGACTTACAGGACAGCGGCAAAATTAAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1627
DB 1561 AGGACTTACAGGACAGCGGCAAAATTAAGCAGCATCAGCCAAACAGGAAATGATTTTAG 1620

QY 1628 CACAAAGATGAGACAAACGAAATGTATTTGCAAAATGTTTCAAAAATGTTTCAAGAGG 1687
DB 1621 CACAAAGATGAGACAAACGAAATGTATTTGCAAAATGTTTCAAAAATGTTTCAAGAGG 1680

QY 1688 CTGGTGGTTTGTATGATGCTGTCCTTCCAACTTGAACGGAATGTACTATCCACAGAGCA 1747
DB 1681 CTGGTGGTTTGTATGATGCTGTCCTTCCAACTTGAACGGAATGTACTATCCACAGAGCA 1740

QY 1748 GAACACAAATTAAGTTTCAACGGCATTTAAATGGTACTATCTGGAAGGCTCAGGCTATTCGCT 1807
DB 1741 GAACACAAATTAAGTTTCAACGGCATTTAAATGGTACTATCTGGAAGGCTCAGGCTATTCGCT 1800

QY 1808 CAGGCCCAACCATGATGATCCGACGAGATTTCTTAAACATCCAGTCCACCTGAGG 1867
DB 1801 CAGGCCCAACCATGATGATCCGACGAGATTTCTTAAACATCCAGTCCACCTGAGG 1860

QY 1868 AACTCTCTCGAATTTTCAAGAGCTTTAAGCCCAAGTGCACCTGAAAGTCAAGGCTGCGCA 1927
DB 1861 AACTCTCTCGAATTTTCAAGAGCTTTAAGCCCAAGTGCACCTGAAAGTCAAGGCTGCGCA 1920

QY 1448 TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGAAAGGAAATGAGGCTTA 1507
Db 1441 TAATCAGCAACGCTATGTGCTTAAATAACACCTTAAAGACTGGAAAGGAAATGAGGCTTA 1500
QY 1508 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGATTCACTTAA 1567
Db 1501 CTCATTGTATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGATTCACTTAA 1560
QY 1568 AGGACTTACAGGGACACCGCGCAAAATAAGCAGCATCAGCAACACAGGAAATGATTTAG 1627
Db 1561 AGGACTTACAGGGACACCGCGCAAAATAAGCAGCATCAGCAACACAGGAAATGATTTAG 1620
QY 1628 CACAAAGGATGAGACAAACGACAAATGTATTTGCAAAATGTTCAAAATGCTCAACAGGAG 1687
Db 1621 CACAAAGGATGAGACAAACGACAAATGTATTTGCAAAATGTTCAAAATGCTCAACAGGAG 1680
QY 1688 CTGGTGTGTTGATGATGTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGCA 1747
Db 1681 CTGGTGTGTTGATGATGTGCTTCCAACTTGAACGGAATGTACTATCCACAGAGCA 1740
QY 1748 GAACACAAATAAGTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1807
Db 1741 GAACACAAATAAGTTCAACGGCAATTAATGGTACTACTGGAAGGCTCAGGCTATTCGCT 1800
QY 1808 CAAGGCCACACCATGATGATCGGACGACAGATTTCTAAACATCCAGTCCACCTGAGG 1867
Db 1801 CAAGGCCACACCATGATGATCGGACGACAGATTTCTAAACATCCAGTCCACCTGAGG 1860
QY 1868 AACTGTCCTGAACTATTTTCAAGACTTAAAGCCTTAAGCCAGTGCACGAAAGTCAACGGCTGCGCA 1927
Db 1861 AACTGTCCTGAACTATTTTCAAGACTTAAAGCCTTAAGCCAGTGCACGAAAGTCAACGGCTGCGCA 1920
QY 1928 CTGTGTCCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1987
Db 1921 CTGTGTCCTCTTCCACACAGAGGGGCTGTGCTCGGTGCTGACGGGACCCACATGCTCCA 1980
QY 1988 GATTAGAGCTGTAAACTTTATCACTTAACTTGATCACTTAAAGCAGCACTTAAAGCAGCAAGCAAGAC 2047
Db 1981 GATTAGAGCTGTAAACTTTATCACTTAACTTGATCACTTAAAGCAGCACTTAAAGCAGCAAGCAAGAC 2040
QY 2048 CTTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2107
Db 2041 CTTAAACATCCATAATTTGATTAGACAGAACACCTATGCAAGATGAACCCGAGGCTGA 2100
QY 2108 GAATCAGACTGACAGTTTACAGACGCTGCTGTACAAACCAAGAAATGTTATGTCAGGTTT 2167
Db 2101 GAATCAGACTGACAGTTTACAGACGCTGCTGTACAAACCAAGAAATGTTATGTCAGGTTT 2160
QY 2168 ATCAGTAAATACTGGAAACAGAACACTTATGTTATACAAATACAGATCATCTTGAAC 2227
Db 2161 ATCAGTAAATACTGGAAACAGAACACTTATGTTATACAAATACAGATCATCTTGAAC 2220
QY 2228 GCATTCCTCTGAGCACTGTTTATACACTGTGAATATACCATATGTCCT 2276
Db 2221 GCATTCCTCTGAGCACTGTTTATACACTGTGAATATACCATATGTCCT 2269

RESULT 14
US-10-789-222-33
; Sequence 33, Application US/10789222
; Publication No. US20040186054A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Qin
; TITLE OF INVENTION: Angiopoietin and Fragments, Mutants, and Analogs Thereof and Uses
; FILE REFERENCE: UPN0003-100 (P3115)
; CURRENT APPLICATION NUMBER: US/10789,222
; CURRENT FILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/450,582
; PRIOR FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 33

; LENGTH: 2269
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-789-222-33
Query Match 99.4%; Score 2269; DB 19; Length 2269;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2269; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 TGGGTTGGTGTATTATCTCTCCACGCTTGGGGAGGGAACAACACTGTAGATCTGGGG 67
Db 1 TGGGTTGGTGTATTATCTCTCCACGCTTGGGGAGGGAACAACACTGTAGATCTGGGG 60
QY 68 AGAGAGGAACAAGACCGTGAAAGCTGCTGTGTAAAAAGCTGACACAGCCCTCCCAAGTG 127
Db 61 AGAGAGGAACAAGACCGTGAAAGCTGCTGTGTAAAAAGCTGACACAGCCCTCCCAAGTG 120
QY 128 AGCAGACTGTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAGAACACAG 187
Db 121 AGCAGACTGTCTTCCCACTGCAATCTGACAGTTTACTGCTGCTGGAGAGAACACAG 180
QY 188 CAGTAAAAACCAAGGTTTGTCTACTGAAAAAGAGGAAGAGACTTTTCATTGACGGACC 247
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QY 1508 CTCATTGTATGAACAACTTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1567
DB |||||
1501 CTCATTGTATGAACAACTTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAA 1560
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Search completed: July 29, 2005, 10:42:15
Job time : 2046.78 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 29, 2005, 02:36:24 ; Search time 2288.57 Seconds
(without alignments)
10777.765 Million cell updates/sec

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Perfect score: 648
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Scoring table: IDENTITY NUC
Gapop 10_0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_est1:
2: gb_est2:
3: gb_hic:
4: gb_est3:
5: gb_est4:
6: gb_est5:
7: gb_est6:
8: gb_gss1:
9: gb_gss2:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	646.4	99.8	1215	9 AY407058	AY407058 Homo sapi
2	646.4	99.8	2134	3 CR620685	CR620685 full-leng
3	635.4	98.1	2083	3 BC022490	BC022490 Homo sapi
4	592.8	91.5	1028	1 AL573084	AL573084 AL573084
5	553.2	85.4	1213	9 AY407059	AY407059 Pan trogl
6	528	81.5	960	5 BX348832	BX348832 BX348832
7	468.8	72.3	1218	9 AY407060	AY407060 Mus muscu
8	468.8	72.3	2443	3 AK048622	AK048622 Mus muscu
9	468.8	72.3	2475	3 AK019860	AK019860 Mus muscu
10	449.4	69.4	487	2 BF760470	BF760470 PM4-CT064
11	442.6	68.3	758	7 CV116084	CV116084 AGENCOURT
12	389	60.0	823	7 CV078760	CV078760 AGENCOURT
13	370.8	57.2	652	7 CF951959	CF951959 UI-M-HLO-
14	353.8	54.6	597	7 CK903582	CK903582 i660e09.Y
15	347.2	53.6	353	1 AA253509	AA253509 zt77c09.i
16	333.8	51.5	561	4 B1962885	B1962885 i659h06.Y
17	323.8	50.0	551	4 B1962932	B1962932 i660e09.Y
18	311.8	48.1	390	2 AW486232	AW486232 71607 MAR
19	304.6	47.0	1014	7 CN646781	CN646781 ILLUMIGEN
20	298.2	46.0	4257	3 AK088439	AK088439 Mus muscu
21	294.2	45.4	634	5 BP307288	BP307288 BP307288
22	277.6	42.8	897	5 BU416193	BU416193 603667484
23	273.2	42.2	800	5 BU171982	BU171982 AGENCOURT
24	272.2	42.0	603	7 CF169608	CF169608 B0815H12-

25	271.2	41.9	806	7 CK474660	CK474660 AGENCOURT
26	267.2	41.2	1056	5 BU131593	BU131593 603119087
27	264	40.7	825	7 CO398106	CO398106 AGENCOURT
28	256.2	39.5	866	7 CN972676	CN972676 20173_124
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30	249	38.4	647	5 BU451988	BU451988 603772372
31	245	37.8	717	7 CK959975	CK959975 4101105 B
32	241.6	37.3	902	5 B0892116	B0892116 AGENCOURT
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36	229	35.3	438	1 AA125751	AA125751 z123401.f
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38	221.2	34.1	715	5 BU284080	BU284080 603865377
39	218.2	33.7	574	7 CN983834	CN983834 52535_126
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44	194.2	30.0	372	7 CN954601	CN954601 2098_41-3
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ALIGNMENTS

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DEFINITION Homo sapiens ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY407058
VERSION AY407058.1 GI:39763029
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1215)
AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2 (bases 1 to 1215)
AUTHORS Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civallo, D.R., Lu, F., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J., Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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RESULT 2
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DEFINITION full-length cDNA clone CS0DI037YG20 of Placenta Cot 25-normalized
of Homo sapiens (human).
ACCESSION CR620685
VERSION CR620685.1 GI:50501492
KEYWORDS HTC; CNSLT cDNA.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2134)
Li.W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 2134)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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FEATURES
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Location/Qualifiers
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/db_xref="taxon:9606"
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/tissue_type="Placenta Cot 25-normalized"
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ORIGIN

Query Match 99.8%; Score 646.4; DB 3; Length 2134;
Best Local Similarity 99.8%; Pred. No. 2.3e-182;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TTCAGAGACTGTGCTGAAGTATTCAAATCAGGACACACAAATGGCATCTACAGTTA 60
Db 1130 TTCAGAGACTGTGCTGAAGTATTCAAATCAGGACACACCAATGGCATCTACAGTTA 1189
QY 61 ACATTCCCTAAATTTCTACAGAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGC 120
Db 1190 ACATTCCCTAAATTTCTACAGAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGGAGC 1249
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Db 1370 TCGCAACTGACTAATCAGCAAGCTGTATGCTTTAAATAACCTTAAAGACTGGGAAGG 1429
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Db 1730 GGCTATTTCGCTCAAGGCCACCAACCATGATGATCCGACAGCAGATTTC 1777

RESULT 3
LOCUS BC022490
DEFINITION Homo sapiens cDNA clone IMAGE:4792831, containing frame-shift
errors.
ACCESSION BC022490
VERSION BC022490.1 GI:18490680
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2083)
Straussberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
```

Klausner, R.D., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D., Altschul, S.F., Zebberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K., Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F., Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L., Stapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L., Scheetz, T.E., Brownstein, M.J., Ussdin, T.B., Toshiyuki, S., Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J., Abramson, R.D., Mullany, S.J., Bosak, S.A., McEwan, P.J., McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S., Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W., Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A., Fahey, J., Helton, E., Kettelman, M., Maman, A., Rodriguez, S., Sanchez, A., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y., Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D., Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M., Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smalls, D.E., Schnerch, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

12477932
2 (bases 1 to 2083)
Director MGC Project.
Direct Submission
Submitted (01-FEB-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgabs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/ILNL at: <http://image.llnl.gov>
Series: IRAC Plate: 32 Row: b Column: 11
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557314
This clone has the following problem: frame shifted.

FEATURES
source
Location/Qualifiers
1..2083
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4792831"
/tissue_type="Brain, hypothalamus"
/clone_lib="NH MGC_96"
/lab_host="DH10B"
/note="vector: pBluescript"

ORIGIN
Query Match 98.1%; Score 635.4; DB 3; Length 2083;
Best Local Similarity 99.7%; Pred. No. 4.5e-179;
Matches 647; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 TTACAGAGACTGTGCTGAAGTATTCAATTCAGGACACACCAATGGCATCTACACGTTA 60
Db 1035 TTACAGAGACTGTGCTGAAGTATTCAATTCAGGACACACCAATGGCATCTACACGTTA 1094
Qy 61 ACATTCCCTTAATTTACAGAGAGATCAAGCCCTACTGTGCATGGAGCTGGAGGAGGC 120
Db 1095 ACATTCCCTTAATTTACAGAGAGATCAAGCCCTACTGTGCATGGAGCTGGAGGAGGC 1154
Qy 121 GGGTGGGCAATTATTTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 180

Db 1155 GGGTGGGCAATTATTTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 1214
Qy 181 GAATATAAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTTGGCTGGAAATAGATTGTT 240
Db 1215 GAATATAAAGTGGGATTTGGTAAACCCCTTCAGGAGAAATATTTGGCTGGAAATAGATTGTT 1274
Qy 241 TCGCAACTGACTAATCAGCAACGCTATGCTTAAATACACCTTAAAGACTGGGAGGG 300
Db 1275 TCGCAACTGACTAATCAGCAACGCTATGCTTAAATACACCTTAAAGACTGGGAGGG 1334
Qy 301 AATGAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGG 360
Db 1335 AATGAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTTATAGG 1394
Qy 361 ATTACACCTTTAAAGGACTTACAGGAGCAGCGCGCAAAATAAGCAGCATCAGCCAAACGAGGA 420
Db 1395 ATTACACCTTTAAAGGACTTACAGGAGCAGCGCGCAAAATAAGCAGCATCAGCCAAACGAGGA 1454
Qy 421 AATGATTTAGCAAAAAGGATGGAGACACAGCAAAATGATTTGCAAAATGTTTCAAAATG 480
Db 1455 AATGATTTAGCAAAAAGGATGGAGACACAGCAAAATGATTTGCAAAATGTTTCAAAATG 1514
Qy 481 CTAACAGGAGGCTGGTGGTTTGATGCATGTGGTCTTCCAACTTGAACGGAATGTACTAT 540
Db 1515 CTAACAGGAGGCTGGTGGTTTGATGCATGTGGTCTTCCAACTTGAACGGAATGTACTAT 1574
Qy 541 CCACAGAG-GCAGAACACAAATAAGTTCAACGGCATTAAATGCTACTTCTGGAAGGCTC 599
Db 1575 CCACAGAGAGCAGACACAAATTAAGTTCAACGGCATTAAATGCTACTTCTGGAAGGCTC 1634
Qy 600 AGCTATTCTGCTCAAGGCCAACACCATGATGATCCGACGAGATTTTC 648
Db 1635 AGCTATTCTGCTCAAGGCCAACACCATGATGATCCGACGAGATTTTC 1683

RESULT 4
AL573084/c
LOCUS
DEFINITION
AL573084 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0D1037YG20 3-PRIME, mRNA sequence.
AL573084
AL573084.3 GI:46246304
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1028)
Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT
On Feb 16, 2001 this sequence version replaced gi:31294447.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 4496.r

For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?s=CS0D1037BD10NPL&c=4496.r>.
Location/Qualifiers
1..1028
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1037YG20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

FEATURES
source
Location/Qualifiers
1..1028
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1037YG20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"

/notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN	
Query Match	91.5%; Score 592.8; DB 1; Length 1028;
Best Local Similarity	96.9%; Pred. No. 2.2e-166;
Matches	628; Conservative 7; Mismatches 9; Indels 4; Gaps 3;
QY	1 TTCCAGAGCTGCTGAAGTATTCATCAATCAGACACACACCAATGGCATCTACAGTTA 60
Db	1002 TTCCAGARCTGGTGTAA--TWTCAATCGACMCAACCAAGT--GCATCTACAG-TW 947
QY	61 ACATTCCTCCATTTTACAGAGAGATCAAGGCTCTGTGACATGGAAGCTGGAGGAGC 120
Db	946 ACATTCCTCCATTTTACAGAGAGATCAAGCCTCTGTAAATGGAAGCTGGAGGAGC 887
QY	121 GGTGGACAAATTTATTCAGGACGTGAGGATGGCAGGCTTTGATTTTCAGAGGACTTGGAAA 180
Db	886 GGTGGACAAATTTATTCAGGACGTGAGGATGGCAGGCTTTGATTTTCAGAGGACTTGGAAA 827
QY	181 GAATATTAAGTGGATTTTGTACCTTTCAGGAGATATTTGCTGGGAATCAGTTGTT 240
Db	826 GAATATTAAGTGGATTTTGTACCTTTCAGGAGATATTTGCTGGGAATCAGTTGTT 767
QY	241 TCGCAACTGACTAATCAGCAAGCTGTATGCTTAAATAACCTTAAAGACTGGGAAGG 300
Db	766 TCGCAACTGACTAATCAGCAAGCTGTATGCTTAAATAACCTTAAAGACTGGGAAGG 707
QY	301 AATGAGCTTACTATTTATGATGAACATTTCTATCTCAAGTGAAGAACTCAATATAGG 360
Db	706 AATGAGCTTACTATTTATGATGAACATTTCTATCTCAAGTGAAGAACTCAATATAGG 647
QY	361 ATTCACTTAAAGGACTTACAGGACAGCGCGCAAAATAGCAGCATCGCCAAACGGA 420
Db	646 ATTCACTTAAAGGACTTACAGGACAGCGCGCAAAATAGCAGCATCGCCAAACGGA 587
QY	421 AATGATTTTATGACAAAGGATGAGACACGCAAAATGTTTGCATAATGTTTCAAAAATG 480
Db	586 AATGATTTTATGACAAAGGATGAGACACGCAAAATGTTTGCATAATGTTTCAAAAATG 527
QY	481 CTAACAGGAGGCTGGTGGTTTATGATGATGCTTCCAACTTGAACGGAATGACTAT 540
Db	526 CTAACAGGAGGCTGGTGGTTTATGATGATGCTTCCAACTTGAACGGAATGACTAT 467
QY	541 CCACAGAGCGCAACACAAATAGTTCAACGCAATTAATGCTACTCTGGAAGGCTCA 600
Db	466 CCACAGAGCGCAACACAAATAGTTCAACGCAATTAATGCTACTCTGGAAGGCTCA 407
QY	601 GGCTATTGCTCAAGGCCCAACACCATGATGATCCGACGAGCATTTTC 648
Db	406 GGCTATTGCTCAAGGCCCAACACCATGATGATCCGACGAGCATTTTC 359

RESULT 5
AY407059
LOCUS
DEFINITION
Pan troglodytes ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION
AY407059
VERSION
AY407059.1
KEYWORDS
GI:39763030
SOURCE
GSS.
ORGANISM
Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
REFERENCE
1 (bases 1 to 1213)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Inferring nonneutral evolution from human-chimp-mouse orthologous

gene trios
Science 302 (5652), 1960-1963 (2003)
14671302
2 (bases 1 to 1213)
Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarawal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J., Adams,M.D. and Cargill,M.
Direct Submission
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering them based on alignment.
FEATURES
Location/Qualifiers
1..1213
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
<1..>1213
/gene="ANGPT2"
/locus_tag="HCM2764"

Query Match	85.4%; Score 553.2; DB 9; Length 1213;
Best Local Similarity	99.5%; Pred. No. 1.8e-154;
Matches	555; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY	91 GCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGAACAATTTTCAGCGAGTGGAGT 150
Db	655 GCCTACTGTGACATGGAAGCTGGAGGAGCGGGTGGAACAATTTTCAGCGAGTGGAGT 714
QY	151 GGCAGCGTTGATTTTTCAGAGGACTTGGAAAGAATAATAAGTGGGATTTTGGTAACCTTCA 210
Db	715 GGCAGCGTTGATTTTTCAGAGGACTTGGAAAGAATAATAAGTGGGATTTTGGTAACCTTCA 774
QY	211 GGAGAATATTCGCTGGGAAATGAGTTTGTTCGCAACTGACTAATCAGCAACGCTATGTG 270
Db	775 GGAGAATATTCGCTGGGAAATGAGTTTGTTCGCAACTGACTAATCAGCAACGCTATGTG 834
QY	271 CTTAAATATACACCTTAAAGACTGGGAAGGAAATGAGGCTTACTCATTTGATGAACATTTT 330
Db	835 CTTAAATATACACCTTAAAGACTGGGAAGGAAATGAGGCTTACTCATTTGATGAACATTTT 894
QY	331 TATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTACAGGGACGCC 390
Db	895 TATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTACAGGGACGCC 954
QY	391 GGCAAAATTAAGCAGCATCAGCCCAACAGGAAATGATTTTAGCAACAAGGATGGAGACAAC 450
Db	955 GGCAAAATTAAGCAGCATCAGCCCAACAGGAAATGATTTTAGCAACAAGGATGGAGACAAC 1014
QY	451 GACAAATGATTTTGCATAATGTTTCAAAATGCTTAAACAGGAGCTGGTGGTTTGTATGTCATGT 510
Db	1015 GACAAATGATTTTGCATAATGTTTCAAAATGCTTAAACAGGAGCTGGTGGTTTGTATGTCATGT 1074
QY	511 GGTCTCTTCCAACTTGAACGGAATGTACTATCCACAGAGCGAGAAACACAAAATAGTTCAAC 570
Db	1075 GGTCTCTTCCAACTTGAACGGAATGTACTATCCACAGAGCGAGAAACACAAAATAGTTCAAC 1134
QY	571 GGCATTAAATGGTACTACTGGAAGGCTCAGGCTATTCGCTCAAGGCCACAAACCATGATG 630
Db	1135 GGCATTAAATGGTACTACTGGAAGGCTCAGGCTATTCGCTCAAGGCCACAAACCATGATG 1194
QY	631 ATCCGACCCAGCAGATTTTC 648
Db	1195 ATCCGACCCAGCAGATTTTC 1212

RESULT 6
BX348832
LOCUS
DEFINITION
Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens CDNA clone CS0DI037YG20 5-PRIME, mRNA sequence.
960 bp
mRNA
linear
EST 08-APR-2004
BX348832
BX348832
clone CS0DI037YG20 5-PRIME, mRNA sequence.

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ACCESSION BX348832
VERSION GI:30365305
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE 1 (bases 1 to 960)
JOURNAL Full-length cDNA libraries and normalization
COMMENT Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
4496.x
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0BAG030ZC09_CS02851_1&c=4496.x

FEATURES
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Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D1037IG20"
/tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 81.5%; Score 528; DB 5; Length 960;
Best Local Similarity 94.7%; Pred. No. 6.2e-147;
Matches 577; Conservative 0; Mismatches 28; Indels 4; Gaps 3;

QY 1 TTCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGGCATCTACACGTTA 60
DB 354 TTCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGGCATCTACACGTTA 413
QY 61 ACATTCCCTTAATCTACAGAGAGATCAAGCCCTCTGTGACATGGAAGCTGGAGGAGGC 120
DB 414 ACATTCCCTTAATCTACAGAGAGATCAAGCCCTCTGTGACATGGAAGCTGGAGGAGGC 473
QY 121 GGGTGGACAATTTTACAGCGACGTGAGTGGCAGCGTTGATTTTCAGAGACTTGGAAA 180
DB 474 GGGTGGACAATTTTACAGCGACGTGAGTGGCAGCGTTGATTTTCAGAGACTTGGAAA 533
QY 181 GAATATAAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTT 240
DB 534 GAATATAAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTT 593
QY 241 TCGCACTGACTAATCAGCAACCGCTATGTGCTTAAATACACCTTAAAGCTGGGAGGG 300
DB 594 TCGCACTGACTAATCAGCAACCGCTATGTGCTTAAATACACCTTAAAGCTGGGAGGG 653
QY 301 AATCAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATTAGG 360
DB 654 AATCAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATTAGG 713
QY 361 ATTCACTTAAAGGACTTACAGGACACCGCGCAAAATTAAGCAGCATCAGCCAAACCGGA 420
DB 714 ATTCACTTAAAGGACTTACAGGACACCGCGCAAAATTAAGCAGCATCAGCCAAACCGGA 772
QY 421 AATGATTTTACGACAAAGGATGGAGACACGACAAATGTTATTTGCAATGTTTCAAAATG 480
DB 773 AATGATTTTACGACAAAGGATGGAGACACGACAAATGTTATTTGCAATGTTTCAAAATG 832

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QY 481 CTAACAGGAGGCTGGT--GGTTTGTATGATGTGGTCTCTTCCAACCTGAACGGAATGACT 538
DB 833 CTAACAGGAGGAGGCTGNTGTTGATGTCATGTTGGTCTTTCACTTGAACGGGATGACT 892
QY 539 ATCCACAGAGGAGGAGACACAAAATAGTTTCAACGGGCATTAATAGTGTACTACTTGGAAAGGCT 598
DB 893 ATCCACAGAGGAGGAGACACCAAC-ATAAGTTCAACGGGCATTAATAGTGTACTACTTGGAAAGTCT 951
QY 599 CAGGCTATT 607
DB 952 ACAGCTTTT 960

RESULT 7
AY407060 1218 bp DNA linear GSS 15-DEC-2003
LOCUS Mus musculus ANGPT2 gene, VIRTUAL TRANSCRIPT, partial sequence,
DEFINITION genomic survey sequence.
ACCESSION AY407060
VERSION AY407060.1 GI:39763031
SOURCE GSS.
ORGANISM Mus musculus (house mouse)
REFERENCE 1 (bases 1 to 1218)
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
AUTHORS Clark,A.G., Gnanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
Perriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
Adams,M.D. and Cargill,M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
COMMENT This sequence was made by sequencing genomic exons and ordering
FEATURES Location/Qualifiers
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/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/genes="ANGPT2"
/locus_tag="HCM2764"

ORIGIN
Query Match 72.3%; Score 468.8; DB 9; Length 1218;
Best Local Similarity 82.7%; Pred. No. 4e-129;
Matches 536; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 TTCAGAGACTGTGCTGAAGTATTCAAAATCAGGACACACCAATGGCATCTACACGTTA 60
DB 568 TTCAGAGACTGTGCGGAAATCTTCAAGTCAGGACTCACCACCGAGCATCTACACTG 627
QY 61 ACATTCCCTTAATCTACAGAGAGATCAAGCCCTTCTGTGACATGGAAGCTGGAGGAGGC 120
DB 628 ACCTTCCCAACTCCACAGAGGAGATCAAGCCCTTCTGTGACATGGAAGCTGGAGGAGGC 687
QY 121 GGGTGGACAATTTATTCAGCGACGTGAGGATGGCAGCGTTGATTTTCAGAGACTTGGAAA 180
DB 688 GGGTGGACAGTCATCCCAACACCCGAGAGATGGCAGTGTGGACTTCCAGAGACCGTGGAAA 747
QY 181 GAATATAAAGTGGGATTTGGTAAACCTTCAGGAGAAATATTGGCTGGGAAATGATTTGTT 240

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Db	748	GAATACAAAGAGGGCTTCGGAGGCCCTCTGGGAGAGTACTGGCTGGCAATGATTTGTGTC	107
QY	241	TCGCAACTGACTAATCAGCAACGCTATGCTTTAAATAACACCTTAAAGACTGGGAAGG	300
Db	808	TCCAGCTGACCGGTGAGCACCGCTAGCTGCTTAAGATCCAGCTGAGACTGGGAGGC	867
QY	301	AATGAGGCTTACTATGTTATGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATTATAGG	360
Db	868	AACGAGCGCATTCGCTGTATGATCACTTCTACCTCGCTGGTGAAGAGTCCAACTACAGG	927
QY	361	ATTCACTTTAAGGACTTACAGGACAGCCGCGGAAATGAAGCAGCATCAGCCACAGCA	420
Db	928	ATTCACTTTACAGGACTCAGCGGACCGCGGAAATGAAGTATCAGCAGCAACACAGCA	987
QY	421	AATGATTTTAGCACAAGGATGAGACAAAGCAACAAATGTTTGCACAAATGTTCAACAATG	480
Db	988	AGTGATTTTAGCACAAGGATTCGGACATGACAAATGATCTGCAAGTGTTCACGATG	1047
QY	481	CTAACAGGAGGCTGTGGTTGATGATGATGTCCTTCCAACTTGAACCGAATGTACTAT	540
Db	1048	CTCTCAGGAGGCTGTGGTTGATGATGATGTCCTTCCAACTTGAACCGAATGTACTAT	1107
QY	541	CCACAGGAGCAGACAAATAGTTTCAAGCGCATTAATGGTACTACTGGAAGGCTCA	600
Db	1108	CCACAAAACAGAAATCAAAATAGTTTAAAGGATCAAGTGTACTACTGGAAGGCTCC	1167
QY	601	GGCTATTGCTCAAGGCGCAACCATGATGATCCGACACGACGATTTTC	648
Db	1168	GCTTACTGCTCAAGGCGCAACCATGATGATCCGACACGATTTTC	1215
RESULT 8			
LOCUS	AK048622	2443 bp mRNA linear HTC 03-APR-2004	
DEFINITION		Mus musculus 16 days embryo head cDNA, RIKEN full-length enriched library, clone: C130089A05 product: ANGIOPOIETIN-2 PRECURSOR, full insert sequence.	
ACCESSION	AK048622		
VERSION	AK048622.1	GI:26339449	
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Mus musculus		
REFERENCE			
AUTHORS	Carninci, P., and Hayashizaki, Y.		
TITLE	High-efficiency full-length cDNA cloning		
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		
MEDLINE	99279253		
PUBMED	10349636		
AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		
JOURNAL	Genome Res. 10 (10), 1617-1630 (2000)		
MEDLINE	20499374		
PUBMED	11042159		
AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Katsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiiwake, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		
TITLE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer		
JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		
MEDLINE	20530913		
PUBMED	11076861		
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the		

TITLE	FANTOM Consortium.
JOURNAL	Functional annotation of a full-length mouse cDNA collection
REFERENCE	Nature 409, 685-690 (2001)
AUTHORS	5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL	Nature 420, 563-573 (2002)
AUTHORS	6 (bases 1 to 2443)
TITLE	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozawa, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.
TITLE	Direct Submission
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan [E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216]
COMMENT	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details. URL: http://genome.gsc.riken.jp/ URL: http://fantom.gsc.riken.jp/ Location/Qualifiers
FEATURES	1..2443
source	/organism="Mus musculus" /mol_type="mRNA" /strain="C57BL/6J" /db_xref="FANTOM DB:C130089A05" /clone="C130089A05" /tissue_type="head" /clone_lib="RIKEN full-length enriched mouse cDNA library" /dev_stage="16 days embryo" 242..1732
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	polyA_site
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Db																						
QY																						
Db																						
QY																						
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274..1784
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match=1488)
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FORTWKEYEGFGLGVEYLNQFVSLQGHRYVLKIQLDKMGNEHAHSLYDFYL
AGEENYRIHLTGLTGTAGKISISIQPGSDFSTKSDNDKICIKCSQMLSGGWFPDCA
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/notes="putative"
polya_site 2475
/notes="putative"

ORIGIN
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Best Local Similarity 82.7%; Pred. No. 5e-129;
Matches 536; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 1 TTCAGAGACTGTGCTGAAGTATTCAAATCAGGACACACCACAAATGGCATCTACAGTTA 60
DB |||
1114 TTCAGAGACTGTGCGGAATCTTCAAGTCAGGACTCACCACCACTGGCATCTACACACTG 1173
QY 61 ACATTCCTTAATTCACAGAGATCAAGGCTTACTGTGACATGGAAGCTGGAGAGGC 120
DB |||
1174 ACCTTCCCCAACTCCACAGAGAGATCAAGGCTTACTGTGACATGACGCTGGGAGGA 1233
QY 121 GGGTGACAAATATTTCAGGCGACTGAGGATGGCAGGTTGATTTTCAGAGGACTTGGAAA 180
DB |||
1234 GGGTGACAGCTCATCCAAACAGGAGAGATGCGAGTGTGACTTCAGAGGACGTGGAAA 1293
QY 181 GAATATAAGTGGGATTTGGTAACCTTCAGGAGAAATATTTGCTGGGAAATCAGTTTGT 240
DB |||
1294 GAATACAAAGAGGGCTTCGGGAGCCCTCTGGGAGAGTACTGCTGGGCAATGAGTTTGT 1353
QY 241 AATGAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGG 360
DB |||
1354 TCCGAGCTGACCGGTGACGACCGCTACGCTTAAAGTCCAGTCAAGGACTGGGAAGGC 1413
QY 301 AATGAGGCTTACTCATTTGATGAACATTTCTATCTCTCAAGTGAAGAACTCAATATAGG 360
DB |||
414 AACGAGCGCATTCGCTGTATGATCACTTCTACCTCGTGGTGAAGTCCAACTACAGG 1473
QY 361 ATTCACTTAAAGGACTTACAGGACAGCCGCAAAATAAGCAGCATCAGCAACACAGGA 420
DB |||
474 ATTCACTTACAGGACTCAGCGGGACCGGGCAAAATAAGTAGCATCAGGCAACACAGGA 1533
QY 421 AATGATTTTAGCACAAGGATGAGACACAGCAATGTATTTGCAATGTTTCACAATG 480
DB |||
1534 AGTGATTTTAGCACAAGGATTCGGACATGAATGAATGATCTCGAAGTGTTCACAGATG 1593
QY 481 CTAACAGGAGGCTGGTGGTTGATGATGCTGTGCTTCCAACTTGAACGGGAATGTACTAT 540
DB |||
1594 CTCTCAGGAGGCTGGTGGTTGACGATGTGTCTTCCAACTTGAATGGACAGTACTAC 1653
QY 541 CCACAGAGCGCAACACAAATAGTTCAACGCCATTAATGTGACTACTCTGGAAGAGGCTCA 600
DB |||
1654 CCACAAAAACAAATACAAATAGTTTAAACGGTATCAAGTGTGACTACTCTGGAAGGGTCC 1713
QY 601 GGCTATTCGCTCAAGGCCCAACCAATGATGATCCGACAGCAGATTTTC 648
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RESULT 10
BF760470/c
LOCUS BF760470
DEFINITION PM4-CT0641-211200-006-e08 CT0641 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF760470
VERSION BF760470.1 GI:12108370
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 487)
Dias Neto,B., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l1=PM4&t2=PM4-CT0641-
211200-006-e08&t3=2000-12-21&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 19
High quality sequence stop: 487.
Location/Qualifiers
1..487
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="CT0641"
/notes="Organ: colon; Vector: puc18; Site_1: Smal; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No.
196,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

FEATURES
source
Query Match 69.4%; Score 449.4; DB 2; Length 487;
Best Local Similarity 98.7%; Pred. No. 2e-123;
Matches 453; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 87 CAAGCCCTACTGTGACATGGAAGCTGGAGAGCGGGGTGGACAATTATTTCAGCGCAGTGA 146
DB |||
484 CACGTGCCATTGTGACATGGAAGCTGGAGAGCGGGGTGGACAATTATTTCAGCGCAGTGA 425
QY 147 GGATGGCAGCGCTGATTTTCAGAGGACTTGAAGAGATATTAAGTGGATTTGGTAACCC 206
DB |||
424 GGATGGCAGCGCTGATTTTCAGAGGACTTGAAGAGATATTAAGTGGATTTGGTAACCC 365
QY 207 TTCAGGAGAAATATTGGCTGGGAAATAGTTTGTTCGCAACTGACTAATCAGCAACGCTA 266
DB |||
364 TTCAGGAGAAATATTGGCTGGGAAATAGTTTGTTCGCAACTGACTAATCAGCAACGCTA 305
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Qy	267	TGTGCTTAAATATACACCTTAAAGACTGGGAAGGAATCAGCGCTTACTCATTTGTATGAACA	326
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Qy	327	TTTCTATCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTTACAGGGAC	386
Db	244	TTTCTACCTCTCAAGTGAAGAACTCAATTTATAGGATTCACCTTAAAGGACTTTACAGGGAC	185
Qy	387	AGCGGGCAAAATAAGCAGCATCAGCCAAACCAAGGAAATGATTTTATAGCACAAAGGATGGAGA	446
Db	184	AGCGGGCAAAATAAGCAGCATCAGCCAAACCAAGGAAATGATTTTATAGCACAAAGGATGGAGA	125
Qy	447	CAACGACAAATGTATTTTGCRAATGTTTCAAAATGCTTAACAGAGGCTGGTGGTTTGATGC	506
Db	124	CAACGACAAATGTATTTTGCRAATGTTTCAAAATGCTTAACAGAGGCTGGTGGTTTGATGC	65
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Db	64	ATGTGGTCTCTTCCAACTTGAACGGAATGTACTATCCACA	26
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LOCUS		758 bp mRNA linear EST 30-AUG-2000	
DEFINITION		AGENCOURT_31522930 NIH_MGC_269 Rattus norvegicus cDNA clone	
		IMAGE:7462299 5', mRNA sequence.	
ACCESSION		CV116084	
VERSION			
KEYWORDS		EST.	
SOURCE		Rattus norvegicus (Norway rat)	
ORGANISM		Rattus norvegicus	
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
		Rattus.	
REFERENCE		1.. (bases 1 to 758)	
AUTHORS		NIH-MGC http://mgc.nci.nih.gov/ .	
TITLE		National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics National Cancer Institute / NCI Bldg. 31 Rm10A07 Bethesda, MD 20892 Email: cgabms-remail.nih.gov Tissue Procurement: Dr. Josef Lazar, Dr. Howard J. Jacob, Medical College of Wisconsin cDNA Library Preparation: Open Biosystems cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM15735 Row: g Column: 01 High quality sequence stop: 594. Location/Qualifiers 1..758 /organism="Rattus norvegicus" /mol_type="mRNA" /db_xref="taxon:10115" /clone="IMAGE:7462299" /tissue_type="whole placenta, 2 pooled" /lab_host="DHI08 Tona" /clone_lib="NIH MGC 269" /note="Organ: placenta; Vector: pExpress-1; Site 1: EcorV Site 2: NotI; Tissue was collected from two pooled placentas from the 21st day of pregnancy. 1st strand cDNA was primed with a Not I - Oligo(dT) primer, double-stranded cDNA was cloned into the Not I and EcorV sites of pExpress-1. Library was size-selected for >1.25 kb fragments for an average insert size of 2.05 kb. A normalized version of this library is also available (NIH MGC 270). Library was constructed by Open Biosystems (Huntsville, AL). Note: this is a Mammalian Gene Collection library"	
FEATURES		source	

Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical College of Wisconsin
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1553 row: p column: 12
High quality sequence stop: 670.
Location/Qualifiers
1. .823
/organism="Rattus norvegicus"
/mol_type="mRNA"
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/clone="IMAGE:7386206"
/lab_host="DH10B Tona"
/clone_lib="NIH MGC 251"
/note="Orymus; thymus; Vector: pExpress-1; Site 1: EcoRV; Site 2: NotI; RNA obtained from testis tissue of 8 wk old animal. Tissues were snap-frozen and kept at -80C before RNA extraction and purification (Tri-reagent method). CDNA was primed using oligo-dT primer:
5'-pGACTAGTCTAGATCGGAGCGCGCC(T)25-3' and cloned into the EcoRV/NotI sites of pExpress-1. Size-selection >1.25kb resulted in an average insert size of 1.6 kb. This primary library is normalized (non-normalized primary library is NIH_MGC_250) and was constructed by Open Biosystems. Note: this is a NIH_MGC library"

FEATURES
source

ORIGIN

Query Match 60.0%; Score 389; DB 7; Length 823;
Best Local Similarity 81.1%; Pred. No. 3.2e-105;
Matches 452; Conservative 0; Mismatches 105; Indels 0; Gaps 0;
QY 92 CTTACTGTGACATGGAAGCTGGAGGAGCGGCTGGACAAATTATTCAGCGACGTGAGGATG 151
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Db 61 GCAGCGTTCATTTTCAGAGGACTTGGAAAGATATTAAGTGGGATTTGTACACCTTCAG 120
QY 212 GAGAAATATGGCTGGGAAATGATTTGTTTCGCAACTGACTAATCAGCAACCTATGTGC 271
Db 121 GAGAGTATTTGGCTGGCAAGAGTTTGTCTCCAGCTGACCAAGTGGGCATCGTACGTGC 180
QY 272 TTAATAATCACCTTAAAGACTGGGAAGGAATGAGGCTTACTCATTTGATGAAACATTTCT 331
Db 181 TGAAGATCCAGCTGAAGGACTGGGAAGGCGAGGACACCTCTCTGTATGAGCACTTCT 240
QY 332 ATCTCTCAAGTGAAGACTCAATATTAGGATTCACCTTAAAGGACTTACAGGACAGCGG 391
Db 241 ACCTGTCCGGCGAGGAGTCAACTACAGGATTCACCTTACAGGACTCAGGACAGCGGG 300
QY 392 GCAAAATAGCAGCATCAGCCCAACAGGAAATGATTTTAGCAAAAGGATGAGCAACG 451
Db 301 GCAAAATAGTACATCAGCCCAACAGGAAATGATTTTAGCAAAAGGATTCGGAATG 360
QY 452 ACAATATGATTTGCAATTTTCAAAATCTCAAAATCTCAAGGAGGCTGGTGGTTGATGATGTG 511
Db 361 ACAATATGATTTGCAATTTTCCAGATGCTCACAGGAGGCTGGTGGTTGATGATGTG 420
QY 512 GTCCCTTCAACTTGAACGGAATGTACTATCCACAGGCGAGCAACAATAGTTTCAACG 571
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QY 572 GCAATTAATGTGTACTCTGAAAGGCTCAGGCTATTTCGCTCAAGGCGCAACACCATCATGA 631
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QY 632 TCCGACCGCAGATTTTC 648
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Db 541 TCCGGCCAGCAGATTTC 557

RESULT 13
CF951959
LOCUS

DEFINITION
UI-M-HL0-GNC-f-02-0-UI.r1 NIH_BMAP_HL0 Mus musculus CDNA clone

ACCESSION
CF951959

KEYWORDS
EST.

SOURCE
Mus musculus (house mouse)

ORGANISM
Mus musculus

REFERENCE
1 (bases 1 to 652)

AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)

TITLE
Unpublished (1999)

JOURNAL
COMMENT

CONTACT: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. James Lin University of Iowa
CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/mouseef.html
This clone was contributed by the Brain Molecular Anatomy Project
(BMAP)

Seq primer: pYX-5.
Location/Qualifiers
1. .652
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/note="Organ: Head; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with NotI and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is CGAAGTGAAT. This library was created for the University
of Iowa Brain Anatomy Project (BMAP): 'Gene Discovery in the
Developing Mouse Nervous System', supported by National
Institute of Mental Health (NIMH)."

FEATURES
source

ORIGIN

Query Match 57.2%; Score 370.8; DB 7; Length 652;
Best Local Similarity 81.6%; Pred. No. 8.7e-100;
Matches 429; Conservative 0; Mismatches 97; Indels 0; Gaps 0;
QY 87 CAAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGCTGGACAAATTATTCAGCGACGTGA 146
Db 127 CCAGGCTTACTGTGACATGGAAGCTGGAGGAGCGGCTGGACAGTCAATCCACACCGAGA 186
QY 147 GGATGGCAGCGTTGATTTTTCAGAGGACTTGGAAAGATATTAAGTGGGATTTGGTAACC 206
Db 187 AGATGGCAGTGTGGACTTCCAGAGGACGCTGGAAAGATATCAAGAGGCGCTTCGGGAGGCC 246
QY 207 TTCAGGAGAAATTTGGCTGGGAAATAGTTTGTTCGCACTGACTATATCAGACAGCTGA 266
Db 247 TCTGGGAGAGTACTGGCTGGGCAATAGTTTGTCTCCAGCTGACCGGTGACACCGCTGA 306
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267 TGTGCTTAAATACACCTTAAAGCTGGGAAGGAATGAGGCTTACTCATTTGTATGACA 326
Db CGTGCTTAAAGATCCAGCTGAATGACTGGGAAGGCAACGAGCGCATTCGCTGTATGATCA 366
Qy TTCTCTATCTCAAGTGAAGCACTCAATATTAGGATTCACCTTAAAGGACTTACAGGGAC 386
Db TTCTCTATCTCAAGTGAAGGCTCAACTACTACAGGATTCACCTTACAGGACTTACAGGGAC 426
Qy AGCCGGCAAAATAGCAGCATCAGCCCAACGAGGAATGATTTTAGCACAAGGATGGAGA 446
Db CGCGGGCAAAATAGTAGCATCAGCCCAACGAGGAATGATTTTAGCACAAGGATTCGGA 486
Qy CAACGACAATATGTTTGGCAATGTTTCAAAATGTTTCAAAATGTTTCAAAATGTTTCAATGC 506
Db CAATGACAATATGTTTGGCAATGTTTCAAAATGTTTCAAAATGTTTCAAAATGTTTCAATGC 546
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Db ATGTGGTCTTCCAACTTGAACGGAATGTTTCAAAATGTTTCAAAATGTTTCAAAATGTTTCAATGC 606
Qy CAACGGCATTAATATGTTTCAAAATGTTTCAAAATGTTTCAAAATGTTTCAAAATGTTTCAATGC 612
Db TAACGGTATCAAGTGGTACTTGAAGGGGTCGCGCTACTCGCTC 652

RESULT 14
CK903582
LOCUS
DEFINITION
is60809.y5 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
cDNA clone IMAGE:5671385 5' similar to TR:O15123 O15123
ANGIOPOIETIN-2. ; mRNA sequence.
CK903582
CK903582.1 GI:45365113
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 597)
Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
McCann,R., Cole,R., Tsagarisshvili,R., Williams,T., Jackson,Y. and
Bowers,Y.
WashU-Harvard Pancreas EST Project
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
This read is a 5' RESEQUENCE of a previously sequenced pancreas
clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco.
Location/Qualifiers
1. 597
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/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA

made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was amplified. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
Plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmid were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN
Query Match 54.6%; Score 353.8; DB 7; Length 597;
Best Local Similarity 99.4%; Pred. No. 1.1e-94;
Matches 355; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 TTCCAGAGACTGTCTGAAATGATTCAATCAGGACACACCAATGCGCATCTACACGTTA 60
Db 241 TTCCAGAGACTGTCTGAAATGATTCAATCAGGACACACCAATGCGCATCTACACGTTA 300
Qy 61 ACATTCCTTAATTCACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGAGGC 120
Db 301 ACATTCCTTAATTCACAGAAGAGATCAAGCCCTACTGTGACATGGAAGCTGGAGGAGGC 360
Qy 121 GGGTGGACAATTAATTCAGGACGCTGAGGATGGGAGGCTGATTTTCAGAGACTTGGAAA 180
Db 361 GGGTGGACAATTAATTCAGGACGCTGAGGATGGGAGGCTGATTTTCAGAGACTTGGAAA 420
Qy 181 GAATATAAAGTGGATTTGGTAACCCCTTCAGGAGATATTTGGCTGGGAAATGAGTTGTT 240
Db 421 GAATATAAAGTGGATTTGGTAACCCCTTCAGGAGATATTTGGCTGGGAAATGAGTTGTT 480
Qy 241 TCGCACTGACTAATCAGCAACGCTATGCTCTTAAATAACACCTTAAAGACTGGGAAGGG 300
Db 481 TCGCACTGACTAATCAGCAACGCTATGCTCTTAAATAACACCTTAAAGACTGGGAAGGG 540
Qy 301 AATGAGCTTACTCATTTGATGATGAACATTTCTATCTCTCAAGTGAAGACTCAATTAT 357
Db 541 AATGAGCTTACTCATTTGATGATGAACATTTCTATCTCTCAAGTGAAGACTCAATTAT 597

RESULT 15
AA253509 353 bp mRNA linear EST 06-AUG-1997
LOCUS
DEFINITION
z777c09.r1 Soares NHMPu S1 Homo sapiens cDNA clone IMAGE:669424 5'
similar to TR:G285989 G285989 ORF, COMPLETE CDS. ; mRNA sequence.
AA253509
AA253509.1 GI:1885684
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 353)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J.,
Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-Merck EST Project 1997
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Insert Length: 879 Std Error: 0.00
Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 309.

FEATURES
source

Location/Qualifiers
1..353
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="GDB:5563391"
/db_xref="taxon:9606"
/clone="IMAGE:669424"
/tissue_type="Pooled human melanocyte, fetal heart, and
pregnant uterus"
/lab_host="DH10B"
/clone_lib="Soares NhMPu S1"
/note="Organ: mixed (see below); Vector: pT73D-Pac
(Pharmacia) with a modified polylinker; Site 1: Not I;
Site 2: Eco RI; Equal amounts of plasmid DNA from three
normalized libraries (melanocyte 2NbHM, pregnant uterus
NbHPU, and fetal heart NbHH19W) were mixed, and ss circles
were made in vitro. Following HAP purification, this DNA
was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from pools of
5,000 clones made from the same 3 libraries. The pools
consisted of I.M.A.G.E. clones 260232-265223,
340488-345479, and 484488-489479."

ORIGIN

Query Match 53.6%; Score 347.2; DB 1; Length 353;
Best Local Similarity 99.1%; Pred. No. 8.7e-93;
Matches 349; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 281 ACCTTAAGACTGGGAGGGAATGAGGCTTACTTCATTGTATGAACATTTCTATCTCTCAA 340
Db 1 ACCTTAAGACTCGGAGGGAATGAGGCTTACTTCATTGTATGAACATTTCTATCTCTCAA 60
QY 341 GTGAAGAATCAATTATAGGATTCACCTTAAAGGACTTACAGGCAGCGGCAAAATAA 400
Db 61 GTGAAGAATCAATTATAGGATTCACCTTAAAGGACTTACAGGCAGCGGCAAAATAA 120
QY 401 GCAGCATCAGCCCAACAGGAATGATTTTGTAGCAAAAGGATCGAGACAAACGAATGTA 460
Db 121 GCAGCATCAGCCCAACAGGAATGATTTTGTAGCAAAAGGATCGAGACAAACGAATGTA 180
QY 461 TTTGCAATGTTCAAAATGCTAACAGGAGGCTGGTGGTTGATGCATGGTCTCTCCA 520
Db 181 TTTGCAATGTTCAAAATGCTAACAGGAGGCTGGTGGTTGATGCATGGTCTCTCCA 240
QY 521 ACTTGAACGGAATGTACTATCCACAGGCGAGAACACAAATAAGTTCAACGGCATTAAAT 580
Db 241 ACTTGAACGGAATGTACTATCCACAGGCGAGAACACAAATAAGTTCAACGGCATTAAAT 300
QY 581 GGTACTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCCAACACCATGATGAT 632
Db 301 GGTACTACTGGAAAGGCTCAGGCTATTTCGCTCAAGGCCCAACACCATGATGAT 352

Search completed: July 29, 2005, 09:49:54
Job time : 2294.57 secs